

Tue Dec 3 12:34:35 2002

us-09-848-868-35.max.rge

Page 1

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on:

December 2, 2002, 12:37:43 ; Search time 2656 Seconds

(without alignments)
197.233 Million cell updates/sec

Title: US-09-848-868-35

Sequence:

1 cccgaagcagctctgac 18

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched:

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_hlg: *
3: gb_in: *
4: gb_com: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_or: *
21: em_ov: *
22: em_pat: *
23: em_pl: *
24: em_pi: *
25: em_ro: *
26: em_sts: *
27: em_un: *
28: em_vl: *
29: em_hlg_hum: *
30: em_hlg_in: *
31: em_hlg_mus: *
32: em_hlg_oth: *
33: em_hlg_pla: *
34: em_hlg_rnd: *
35: em_hlg_wrt: *
36: em_hlg_vrt: *
37: em_hlg_vrt: *
38: em_hlg_vrt: *
39: em_hlg_vrt: *
40: em_hlg_vrt: *
41: em_hlg_vrt: *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	6	AX298039 Sequence
2	17	100.0	36	6	AX298040 Sequence
3	17	94.4	28	6	106689 Sequence
4	15	83.3	25	6	AR003360 Sequence
5	14.6	82.2	26	6	AX053071 Sequence
6	13.2	73.3	21	6	AX464857 Sequence
7	13.2	73.3	27	6	AX464857 Sequence
8	12.4	68.9	26	6	AR137946 Sequence
9	12.2	67.8	17	6	AX348011 Sequence
10	12.2	67.8	20	6	AR174377 Sequence
11	12.2	67.8	23	6	E10818 Sequence
12	12.2	67.8	26	6	AR066373 Sequence
13	12.2	67.8	33	6	AX004559 Sequence
14	12.2	67.8	33	6	AX004579 Sequence
15	12.2	67.8	33	6	AX036550 Sequence
16	12.2	67.8	30	6	AX127337 Sequence
17	12.2	66.7	22	6	AR095087 Sequence
18	12.2	66.7	23	6	AR095087 Sequence
19	12.2	66.7	23	6	AR095087 Sequence
20	12.2	66.7	24	6	AR095087 Sequence
21	12.2	66.7	26	6	AR108592 Sequence
22	12.2	66.7	26	6	BD012014 Sequence
23	12.2	66.7	26	6	E55063 Sequence
24	12.2	66.7	26	6	BD012014 Sequence
25	12.2	66.7	26	6	BD012014 Sequence
26	12.2	66.7	28	6	BD012014 Sequence
27	12.2	66.7	28	6	BD012014 Sequence
28	12.2	66.7	28	6	BD012014 Sequence
29	12.2	66.7	28	6	BD012014 Sequence
30	12.2	66.7	28	6	BD012014 Sequence
31	12.2	66.7	28	6	BD012014 Sequence
32	12.2	66.7	28	6	BD012014 Sequence
33	12.2	66.7	28	6	BD012014 Sequence
34	12.2	66.7	28	6	BD012014 Sequence
35	12.2	66.7	28	6	BD012014 Sequence
36	12.2	66.7	28	6	BD012014 Sequence
37	12.2	66.7	28	6	BD012014 Sequence
38	12.2	66.7	28	6	BD012014 Sequence
39	12.2	66.7	28	6	BD012014 Sequence
40	12.2	66.7	28	6	BD012014 Sequence
41	12.2	66.7	28	6	BD012014 Sequence

C 66	11.2	62.2	21	6	AX119946	AX119946 Sequence	139	10.8	60.0	20	6	AR212409	AR212409 Sequence
C 67	11.2	62.2	24	6	AX111721	AX111721 Sequence	140	10.8	60.0	21	6	AR175671	AR175671 Sequence
C 68	11.2	62.2	24	6	AX111724	AX111724 Sequence	141	10.8	60.0	21	6	AR195247	AR195247 Sequence
C 69	11.2	62.2	24	6	AX148205	AX148205 Sequence	142	10.8	60.0	21	6	AX097226	AX097226 Sequence
C 70	11.2	62.2	24	6	AX148265	AX148265 Sequence	143	10.8	60.0	21	6	AX487105	AX487105 Sequence
C 71	11.2	62.2	24	6	AX119033	AX119033 Sequence	144	10.8	60.0	21	12	ASE251794	ASE251794
C 72	11.2	62.2	24	6	AX447009	AX447009 Sequence	145	10.8	60.0	22	6	AR173407	AR173407 Sequence
C 73	11.2	62.2	24	6	BD004779	BD004779 Novel VEG	146	10.8	60.0	22	6	AX097573	AX097573 Sequence
C 74	11.2	62.2	24	6	E38430	E38430 Novel polyp	147	10.8	60.0	23	6	AX426955	AX426955 Sequence
C 75	11.2	62.2	25	6	AR124224	AR124224 Sequence	148	10.8	60.0	24	6	AX088203	AX088203 Sequence
C 76	11.2	62.2	25	6	AR210217	AR210217 Sequence	149	10.8	60.0	25	6	AX278911	AX278911 Sequence
C 77	11.2	62.2	25	6	AR210235	AR210235 Sequence	150	10.8	60.0	25	6	AX426975	AX426975 Sequence
C 78	11.2	62.2	25	6	AX402645	AX402645 Sequence	151	10.8	60.0	26	6	AX037848	AX037848 Sequence
C 79	11.2	62.2	27	6	AX402663	AX402663 Sequence	152	10.8	60.0	26	6	AX466921	AX466921 Sequence
C 80	11.2	62.2	27	6	AR087804	AR087804 Sequence	153	10.8	60.0	26	6	I13498	I13498 Sequence
C 81	11.2	62.2	27	6	AR159648	AR159648 Sequence	154	10.8	60.0	28	6	AR090720	AR090720 Sequence
C 82	11.2	62.2	28	6	AX092072	AX092072 Sequence	155	10.8	60.0	28	6	AR197755	AR197755 Sequence
C 83	11.2	62.2	28	6	AX092090	AX092090 Sequence	156	10.8	60.0	30	6	AR079829	AR079829 Sequence
C 84	11.2	62.2	28	6	AX092173	AX092173 Sequence	157	10.8	60.0	30	6	AX253354	AX253354 Sequence
C 85	11.2	62.2	28	6	AX092896	AX092896 Sequence	158	10.8	60.0	30	6	AX253362	AX253362 Sequence
C 86	11.2	62.2	28	6	I89994	I89994 Sequence	159	10.8	60.0	31	6	AX425508	AX425508 Sequence
C 87	11.2	62.2	29	6	A39955	A39955 Sequence	160	10.8	60.0	32	6	A25771	A25771 sense oligo
C 88	11.2	62.2	29	6	AR054427	AR054427 Sequence	161	10.8	60.0	32	6	AX030669	AX030669 Sequence
C 89	11.2	62.2	29	6	AR167240	AR167240 Sequence	162	10.8	60.0	32	6	I30310	I30310 Sequence
C 90	11.2	62.2	30	6	AX287625	AX287625 Sequence	163	10.8	60.0	34	6	AR179179	AR179179 Sequence
C 91	11.2	62.2	30	6	E32674	E32674 Peptide inh	164	10.8	60.0	36	6	AR183895	AR183895 Sequence
C 92	11.2	62.2	32	6	AX402994	AX402994 Sequence	165	10.8	60.0	36	6	I08440	I08440 Sequence
C 93	11.2	62.2	32	6	BD011320	BD011320 Human tel	166	10.8	60.0	37	6	AX185857	AX185857 Sequence
C 94	11.2	62.2	32	6	E37069	E37069 Human telom	167	10.8	60.0	40	6	AR169568	AR169568 Sequence
C 95	11.2	62.2	34	6	AX019301	AX019301 Sequence	168	10.8	60.0	40	6	AR183894	AR183894 Sequence
C 96	11.2	62.2	34	6	AX033754	AX033754 Sequence	169	10.8	60.0	40	6	AX018529	AX018529 Sequence
C 97	11.2	62.2	36	6	AR036037	AR036037 Sequence	170	10.8	60.0	40	6	AX018605	AX018605 Sequence
C 98	11.2	62.2	36	6	AR161823	AR161823 Sequence	171	10.8	60.0	40	6	I08439	I08439 Sequence
C 99	11.2	62.2	36	6	AR161834	AR161834 Sequence	172	10.8	60.0	41	6	A38942	A38942 Sequence
C 100	11.2	62.2	36	6	AX378847	AX378847 Sequence	173	10.8	60.0	41	6	AR054338	AR054338 Sequence
C 101	11.2	62.2	36	6	AX378848	AX378848 Sequence	174	10.8	60.0	41	6	AX004844	AX004844 Sequence
C 102	11.2	62.2	36	6	I85715	I85715 Sequence	175	10.8	60.0	42	6	A05118	A05118
C 103	11.2	62.2	38	6	AX203574	AX203574 Sequence	176	10.8	60.0	42	6	A33007	A33007
C 104	11.2	62.2	41	6	AX004845	AX004845 Sequence	177	10.8	60.0	42	6	A33008	A33008
C 105	11.2	62.2	41	6	BD007098	BD007098 Targeted	178	10.8	60.0	42	6	A33012	A33012 Synthetic P
C 106	11.2	62.2	42	6	AR024300	AR024300 Sequence	179	10.8	60.0	42	6	AX357177	AX357177 Sequence
C 107	11.2	62.2	42	6	AR045153	AR045153 Sequence	180	10.8	60.0	42	6	AX357178	AX357178 Sequence
C 108	11.2	62.2	42	6	AR069547	AR069547 Sequence	181	10.8	60.0	42	6	AX357182	AX357182 Sequence
C 109	11.2	62.2	42	6	BD011377	BD011377 Chimeric	182	10.8	60.0	43	6	AX297642	AX297642 Sequence
C 110	11.2	62.2	42	6	E16947	E16947 PCR primer	183	10.8	60.0	48	6	A34134	A34134
C 111	11.2	62.2	42	6	E43847	E43847 Chimeric an	184	10.8	60.0	48	6	A35389	A35389
C 112	11.2	62.2	44	6	AX297515	AX297515 Sequence	185	10.8	60.0	48	6	A38198	A38198
C 113	11.2	62.2	45	6	A03928	A03928 Nucleotide	186	10.8	60.0	48	6	A61805	A61805
C 114	11.2	62.2	45	6	A03939	A03939 Nucleotide	187	10.8	60.0	50	6	AR071104	AR071104 Sequence
C 115	11.2	62.2	45	6	A31934	A31934 H.sapiens M	188	10.8	60.0	50	6	AX157852	AX157852 Sequence
C 116	11.2	62.2	48	6	A38199	A38199 Sequence	189	10.8	60.0	50	6	AX158942	AX158942 Sequence
C 117	11.2	62.2	50	6	AX160204	AX160204 Sequence	190	10.8	60.0	50	6	AX159544	AX159544 Sequence
C 118	11.2	62.2	50	6	AR192514	AR192514 Sequence	191	10.8	58.9	18	6	AR154548	AR154548 Sequence
C 119	11.2	62.2	18	6	AR192910	AR192910 Sequence	192	10.6	58.9	18	6	E40623	E40623 RNA virus S
C 120	11.2	62.2	20	6	AR126707	AR126707 Sequence	193	10.6	58.9	19	6	AR154549	AR154549 Sequence
C 121	11.2	62.2	20	6	E15901	E15901 Primer	194	10.6	58.9	19	6	AX001207	AX001207 Sequence
C 122	11.2	62.2	21	6	AX095173	AX095173 Sequence	195	10.6	58.9	19	6	AX001209	AX001209 Sequence
C 123	11.2	62.2	27	6	AX179395	AX179395 Sequence	196	10.6	58.9	19	6	AX268649	AX268649 Sequence
C 124	11.2	62.2	31	6	AX259869	AX259869 Sequence	197	10.6	58.9	19	6	AX353624	AX353624 Sequence
C 125	11.2	62.2	31	6	BD002774	BD002774 Gene comp	198	10.6	58.9	19	6	AX353626	AX353626 Sequence
C 126	11.2	62.2	38	6	AR046422	AR046422 Sequence	199	10.6	58.9	19	6	AX393525	AX393525 Sequence
C 127	11.2	62.2	38	6	I53474	I53474 Sequence	200	10.6	58.9	20	6	A07598	A07598
C 128	11.2	62.2	40	6	I00292	I00292 Sequence	201	10.6	58.9	20	6	AR062641	AR062641 Sequence
C 129	11.2	62.2	42	6	AR032389	AR032389 Sequence	202	10.6	58.9	20	6	AR080260	AR080260 Sequence
C 130	11.2	62.2	42	6	AR209053	AR209053 Sequence	203	10.6	58.9	20	6	AR094445	AR094445 Sequence
C 131	11.2	62.2	42	6	I29129	I29129 Sequence	204	10.6	58.9	20	6	AR104744	AR104744 Sequence
C 132	11.2	62.2	42	6	I90803	I90803 Sequence	205	10.6	58.9	20	6	AR105566	AR105566 Sequence
C 133	10.8	60.0	16	6	AX402876	AX402876 Sequence	206	10.6	58.9	20	6	AR123228	AR123228 Sequence
C 134	10.8	60.0	17	6	AR190541	AR190541 Sequence	207	10.6	58.9	20	6	AR168600	AR168600 Sequence
C 135	10.8	60.0	17	6	AR190542	AR190542 Sequence	208	10.6	58.9	20	6	AX201725	AX201725 Sequence
C 136	10.8	60.0	17	6	AX422274	AX422274 Sequence	209	10.6	58.9	20	6	AX292874	AX292874 Sequence
C 137	10.8	60.0	17	6	AX423069	AX423069 Sequence	210	10.6	58.9	20	6	I20643	I20643
C 138	10.8	60.0	20	6	AR174378	AR174378 Sequence	211	10.6	58.9	20	6	I33336	I33336

C 212	10.6	58.9	21	6	A48993	AA8993 Sequence 5	285	10.6	58.9	47	6	AR058387	AR058387 Sequence
C 213	10.6	58.9	21	6	A87853	AR7853 Sequence 1	286	10.6	58.9	47	6	AR088213	AR088213 Sequence
C 214	10.6	58.9	21	6	A89820	AR9820 Sequence 1	287	10.6	58.9	47	6	AX194735	AX194735 Sequence
C 215	10.6	58.9	21	6	AR076438	AR076438 Sequence	288	10.6	58.9	48	6	E13196	E13196 Oligonucleo
C 216	10.6	58.9	21	6	AR147757	AR147757 Sequence	289	10.6	58.9	49	6	AX144981	AX144981 Sequence
C 217	10.6	58.9	21	6	AR154542	AR154542 Sequence	290	10.6	58.9	49	6	AX050469	AX050469 Sequence
C 218	10.6	58.9	21	6	AX056828	AX056828 Sequence	291	10.6	58.9	49	6	108628	108628 Sequence 29
C 219	10.6	58.9	21	6	AX476968	AX476968 Sequence	292	10.6	58.9	50	6	AX159200	AX159200 Sequence
C 220	10.6	58.9	21	6	I34621	I34621 Sequence 8	293	10.6	58.9	50	6	AX164949	AX164949 Sequence
C 221	10.6	58.9	22	6	AR102184	AR102184 Sequence	294	10.6	58.9	50	6	AX202538	AX202538 Sequence
C 222	10.6	58.9	22	6	AR204438	AR204438 Sequence	295	10.6	58.9	50	10	MM078813	MM078813 Mus musculu
C 223	10.6	58.9	23	6	A24437	AA2437 Oligonucleo	296	10.4	57.8	15	6	AR041381	AR041381 Sequence
C 224	10.6	58.9	23	6	AR036973	AR036973 Sequence	297	10.4	57.8	15	6	AR056170	AR056170 Sequence
C 225	10.6	58.9	24	6	AR034498	AR034498 Sequence	298	10.4	57.8	15	6	AR113928	AR113928 Sequence
C 226	10.6	58.9	24	6	AR048598	AR048598 Sequence	299	10.4	57.8	18	6	A26518	A26518
C 227	10.6	58.9	24	6	AX288211	AX288211 Sequence	300	10.4	57.8	18	6	AR012652	AR012652
C 228	10.6	58.9	24	6	AX447031	AX447031 Sequence	301	10.4	57.8	18	6	AR064291	AR064291 Sequence
C 229	10.6	58.9	24	6	E58780	E58780 Novel human	302	10.4	57.8	18	6	AR067049	AR067049 Sequence
C 230	10.6	58.9	24	6	I34302	I34302 Sequence 7	303	10.4	57.8	18	6	AR096782	AR096782 Sequence
C 231	10.6	58.9	26	6	A14855	A14855 Nucleotide	304	10.4	57.8	18	6	AX020707	AX020707 Sequence
C 232	10.6	58.9	26	6	AR000039	AR000039 Sequence	305	10.4	57.8	20	6	AR004680	AR004680 Sequence
C 233	10.6	58.9	26	6	AR090896	AR090896 Sequence	306	10.4	57.8	20	6	AR008166	AR008166 Sequence
C 234	10.6	58.9	26	6	AR197931	AR197931 Sequence	307	10.4	57.8	20	6	AR067269	AR067269 Sequence
C 235	10.6	58.9	27	6	A45806	A45806 Sequence 44	308	10.4	57.8	20	6	AR100497	AR100497 Sequence
C 236	10.6	58.9	27	6	AX003575	AX003575 Sequence 25	309	10.4	57.8	20	6	AR136949	AR136949 Sequence
C 237	10.6	58.9	30	6	A97525	A97525 Sequence	310	10.4	57.8	20	6	AR150152	AR150152
C 238	10.6	58.9	30	6	AR048786	AR048786 Sequence	311	10.4	57.8	20	6	AR150304	AR150304 Sequence
C 239	10.6	58.9	30	6	AR097637	AR097637 Sequence	312	10.4	57.8	20	6	AR162585	AR162585
C 240	10.6	58.9	30	6	AR103227	AR103227 Sequence	313	10.4	57.8	20	6	AR163917	AR163917 Sequence
C 241	10.6	58.9	30	6	AX287139	AX287139 Sequence	314	10.4	57.8	20	6	AX117238	AX117238 Sequence
C 242	10.6	58.9	30	6	I12895	I12895 Sequence 2	315	10.4	57.8	20	6	AX402890	AX402890 Sequence
C 243	10.6	58.9	30	6	I56893	I56893 Sequence 2	316	10.4	57.8	20	6	I76950	I76950 Sequence 9
C 244	10.6	58.9	30	6	I88163	I88163 Sequence 2	317	10.4	57.8	20	6	I76950	I76950 Sequence 9
C 245	10.6	58.9	31	6	AX248490	AX248490 Sequence	318	10.4	57.8	20	6	I81041	I81041 Sequence 9
C 246	10.6	58.9	31	6	AR081874	AR081874 Sequence	319	10.4	57.8	21	6	AR148291	AR148291 Sequence
C 247	10.6	58.9	34	6	I34949	I34949 Sequence 35	320	10.4	57.8	21	6	AX097213	AX097213 Sequence
C 248	10.6	58.9	35	6	AX162532	AX162532 Sequence	321	10.4	57.8	22	6	AX072227	AX072227 Sequence
C 249	10.6	58.9	37	6	AR063476	AR063476 Sequence	322	10.4	57.8	22	6	I26338	I26338
C 250	10.6	58.9	37	6	I28156	I28156 Sequence 13	323	10.4	57.8	23	6	A27196	A27196
C 251	10.6	58.9	38	6	AR058958	AR058958 Sequence	324	10.4	57.8	23	6	A29358	A29358
C 252	10.6	58.9	38	6	AR105232	AR105232 Sequence	325	10.4	57.8	23	6	AR077342	AR077342 Sequence
C 253	10.6	58.9	38	6	AR119153	AR119153 Sequence	326	10.4	57.8	23	6	AR105708	AR105708 Sequence
C 254	10.6	58.9	38	6	AR123524	AR123524 Sequence	327	10.4	57.8	23	6	AR117962	AR117962 Sequence
C 255	10.6	58.9	38	6	AR138177	AR138177 Sequence	328	10.4	57.8	23	6	AX010544	AX010544 Sequence
C 256	10.6	58.9	38	6	AR176738	AR176738 Sequence	329	10.4	57.8	23	6	AX166704	AX166704 Sequence
C 257	10.6	58.9	38	6	AR198309	AR198309 Sequence	330	10.4	57.8	23	6	AX357137	AX357137 Sequence
C 258	10.6	58.9	38	6	AX470002	AX470002 Sequence	331	10.4	57.8	23	6	AX376781	AX376781 Sequence
C 259	10.6	58.9	40	6	A19014	A19014 Oligonucleo	332	10.4	57.8	23	6	EO9109	EO9109 Synthetic O
C 260	10.6	58.9	41	6	AR061383	AR061383 Sequence	333	10.4	57.8	23	6	I27517	I27517 Sequence 31
C 261	10.6	58.9	41	6	AR108282	AR108282 Sequence	334	10.4	57.8	23	6	I56683	I56683 Sequence 11
C 262	10.6	58.9	41	6	AX404879	AX404879 Sequence	335	10.4	57.8	24	6	AR090687	AR090687 Sequence
C 263	10.6	58.9	41	6	I16239	I16239 Sequence 65	336	10.4	57.8	24	6	AR197722	AR197722 Sequence
C 264	10.6	58.9	41	6	I66725	I66725 Sequence 65	337	10.4	57.8	24	6	AX445250	AX445250 Sequence
C 265	10.6	58.9	41	6	I84819	I84819 Sequence 65	338	10.4	57.8	24	6	E25701	E25701 Animal with
C 266	10.6	58.9	42	6	A06938	A06938 F.domesticu	339	10.4	57.8	25	6	AR165844	AR165844 Sequence
C 267	10.6	58.9	42	6	AR011352	AR011352 Sequence	340	10.4	57.8	25	6	AR165845	AR165845 Sequence
C 268	10.6	58.9	42	6	AR061012	AR061012 Sequence	341	10.4	57.8	25	6	AR165845	AR165845 Sequence
C 269	10.6	58.9	42	6	AR061016	AR061016 Sequence	342	10.4	57.8	25	6	AR169623	AR169623 Sequence
C 270	10.6	58.9	42	6	AR079772	AR079772 Sequence	343	10.4	57.8	25	6	AX188494	AX188494 Sequence
C 271	10.6	58.9	42	6	AR081302	AR081302 Sequence	344	10.4	57.8	28	6	AX188430	AX188430 Sequence
C 272	10.6	58.9	42	6	AR170662	AR170662 Sequence	345	10.4	57.8	31	6	AX247968	AX247968 Sequence
C 273	10.6	58.9	42	6	AX018723	AX018723 Sequence	346	10.4	57.8	31	6	AX248003	AX248003 Sequence
C 274	10.6	58.9	42	6	AX018726	AX018726 Sequence	347	10.4	57.8	31	6	AX248159	AX248159 Sequence
C 275	10.6	58.9	42	6	AX418351	AX418351 Sequence	348	10.4	57.8	31	6	AX249255	AX249255 Sequence
C 276	10.6	58.9	44	6	I17990	I17990 Sequence 22	349	10.4	57.8	31	6	AX249675	AX249675 Sequence
C 277	10.6	58.9	44	6	AR002174	AR002174 Sequence	350	10.4	57.8	31	6	BD002343	BD002343 Gene comp
C 278	10.6	58.9	44	6	AX202534	AX202534 Sequence	351	10.4	57.8	35	6	AX188424	AX188424 Sequence
C 279	10.6	58.9	44	6	AR035926	AR035926 Sequence	352	10.4	57.8	35	6	AR057075	AR057075 Sequence
C 280	10.6	58.9	45	6	I20162	I20162 Sequence 11	353	10.4	57.8	36	6	AR095675	AR095675 Sequence
C 281	10.6	58.9	46	6	AX111206	AX111206 Sequence	354	10.4	57.8	36	6	AR114833	AR114833 Sequence
C 282	10.6	58.9	47	6	AR013893	AR013893 Sequence	355	10.4	57.8	37	6	AX092843	AX092843 Sequence
C 283	10.6	58.9	47	6	AR033847	AR033847 Sequence	356	10.4	57.8	38	6	A27205	A27205 Oligonucleo
C 284	10.6	58.9	47	6	AR042507	AR042507 Sequence	357	10.4	57.8	38	6	A33846	A33846 Synthetic p

358	10.4	57.8	38	6	AR046406	AR046406 Sequence	431	10.2	56.7	27	6	AX343652	AX343652 Sequence
359	10.4	57.8	38	6	AR046426	AR046426 Sequence	432	10.2	56.7	28	6	AR089366	AR089366 Sequence
360	10.4	57.8	38	6	AR057835	AR057835 Sequence	433	10.2	56.7	28	6	AR093566	AR093566 Sequence
361	10.4	57.8	38	6	AR115593	AR115593 Sequence	434	10.2	56.7	28	6	AR136052	AR136052 Sequence
362	10.4	57.8	38	6	BD001863	BD001863 Method fo	435	10.2	56.7	28	6	AX282010	AX282010 Sequence
363	10.4	57.8	38	6	I27530	Sequence 44	436	10.2	56.7	28	6	BD007566	BD007566 Process O
364	10.4	57.8	38	6	I53458	Sequence 11	437	10.2	56.7	29	6	AR3793	AR3793 Sequence 4
365	10.4	57.8	38	6	I53478	Sequence 12	438	10.2	56.7	29	6	AR059355	AR059355 Sequence
366	10.4	57.8	40	6	AR125309	Sequence	439	10.2	56.7	29	6	AR071631	AR071631 Sequence
367	10.4	57.8	47	6	AX004826	Sequence	440	10.2	56.7	29	6	AX188737	AX188737 Sequence
368	10.4	57.8	50	6	AR088341	Sequence	441	10.2	56.7	29	6	AX188745	AX188745 Sequence
369	10.4	57.8	50	6	AR088342	Sequence	442	10.2	56.7	29	6	E11314	E11314 PCR primer
370	10.4	57.8	50	6	AR117933	Sequence	443	10.2	56.7	29	6	E11315	E11315 PCR primer
371	10.4	57.8	50	6	AR117951	Sequence	444	10.2	56.7	30	6	I52059	I52059 Sequence 1
372	10.2	56.7	16	6	AR154543	Sequence	445	10.2	56.7	30	6	A32442	A32442 p12 cloning
373	10.2	56.7	17	6	AR154547	Sequence	446	10.2	56.7	30	6	AX282016	AX282016 Sequence
374	10.2	56.7	17	6	AR191757	Sequence	447	10.2	56.7	30	6	AX282020	AX282020 Sequence
375	10.2	56.7	18	6	AR8005	Sequence 35	448	10.2	56.7	31	6	AX033342	AX033342 Sequence
376	10.2	56.7	18	6	AR192809	Sequence	449	10.2	56.7	31	6	AX248630	AX248630 Sequence
377	10.2	56.7	19	6	AR086960	Sequence	450	10.2	56.7	31	6	BD002754	BD002754 Gene comp
378	10.2	56.7	19	6	AX179542	Sequence	451	10.2	56.7	31	6	E25833	E25833 Method for
379	10.2	56.7	19	6	AX226036	Sequence	452	10.2	56.7	32	6	A18274	A18274 oligonucleo
380	10.2	56.7	19	6	AX226037	Sequence	453	10.2	56.7	32	6	AR069600	AR069600 Sequence
381	10.2	56.7	19	6	I84460	Sequence 1	454	10.2	56.7	32	6	AR069603	AR069603 Sequence
382	10.2	56.7	20	6	A36292	Sequence 15	455	10.2	56.7	32	6	AX188719	AX188719 Sequence
383	10.2	56.7	20	6	AR062664	Sequence	456	10.2	56.7	32	6	AX306632	AX306632 Sequence
384	10.2	56.7	20	6	AR104767	Sequence	457	10.2	56.7	32	6	I15742	I15742 Sequence 8
385	10.2	56.7	20	6	AR105589	Sequence	458	10.2	56.7	33	6	AR152548	AR152548 Sequence
386	10.2	56.7	20	6	AR121074	Sequence	459	10.2	56.7	33	6	AX031406	AX031406 Sequence
387	10.2	56.7	20	6	AR123251	Sequence	460	10.2	56.7	33	6	I31032	I31032 Sequence 64
388	10.2	56.7	20	6	AR162355	Sequence	461	10.2	56.7	33	13	AX031516	AX031516 Sequence
389	10.2	56.7	20	6	AR211292	Sequence	462	10.2	56.7	34	6	AR073546	AR073546 Sequence
390	10.2	56.7	20	6	AX076196	Sequence	463	10.2	56.7	34	6	AX033207	AX033207 Sequence
391	10.2	56.7	20	6	AX194390	Sequence	464	10.2	56.7	34	6	I20488	I20488 Sequence 10
392	10.2	56.7	20	6	AX293085	Sequence	465	10.2	56.7	36	6	AR136044	AR136044 Sequence
393	10.2	56.7	20	6	AX294251	Sequence	466	10.2	56.7	36	6	AR136069	AR136069 Sequence
394	10.2	56.7	20	6	AX296272	Sequence	467	10.2	56.7	36	6	AR203924	AR203924 Sequence
395	10.2	56.7	20	6	AX371349	Sequence	468	10.2	56.7	36	6	AX049403	AX049403 Sequence
396	10.2	56.7	20	6	AX403130	Sequence	469	10.2	56.7	36	6	AX053075	AX053075 Sequence
397	10.2	56.7	20	6	AX453030	Sequence	470	10.2	56.7	36	6	AX085425	AX085425 Sequence
398	10.2	56.7	20	6	BD011252	Sequence	471	10.2	56.7	36	6	AX268692	AX268692 Sequence
399	10.2	56.7	20	6	E37001	Human telom	472	10.2	56.7	36	6	BD007558	BD007558 Process O
400	10.2	56.7	20	6	I20666	Sequence 64	473	10.2	56.7	36	6	BD007583	BD007583 Process O
401	10.2	56.7	20	6	I33359	Sequence 64	474	10.2	56.7	37	6	AR048870	AR048870 Sequence
402	10.2	56.7	20	6	I83392	Sequence 15	475	10.2	56.7	38	6	AX378841	AX378841 Sequence
403	10.2	56.7	21	6	AR091658	Sequence	476	10.2	56.7	38	6	AX378842	AX378842 Sequence
404	10.2	56.7	21	6	AR137952	Sequence	477	10.2	56.7	40	6	AR149456	AR149456 Sequence
405	10.2	56.7	21	6	AX095232	Sequence	478	10.2	56.7	40	6	AX356280	AX356280 Sequence
406	10.2	56.7	21	6	AX095687	Sequence	479	10.2	56.7	40	6	E94928	E94928 Method for
407	10.2	56.7	21	6	AX322557	Sequence	480	10.2	56.7	41	6	BD009289	BD009289 Mutant pe
408	10.2	56.7	22	6	I81383	Sequence 9	481	10.2	56.7	42	6	AX085431	AX085431 Sequence
409	10.2	56.7	23	6	A62922	Sequence 16	482	10.2	56.7	43	6	A05113	A05113 Oligonucleo
410	10.2	56.7	23	6	AX088725	Sequence	483	10.2	56.7	44	6	I38535	I38535 Sequence 3
411	10.2	56.7	23	6	AX088726	Sequence	484	10.2	56.7	44	9	HMSPARC01	M27337 Human ostreo
412	10.2	56.7	24	6	AR175963	Sequence	485	10.2	56.7	45	6	AX201009	AX201009 Sequence
413	10.2	56.7	24	6	AX098725	Sequence	486	10.2	56.7	45	6	AX267808	AX267808 Sequence
414	10.2	56.7	24	6	AX136953	Sequence	487	10.2	56.7	45	6	I26650	I26650 Sequence 17
415	10.2	56.7	24	6	AX288452	Sequence	488	10.2	56.7	50	1	PSECLPBA	L06014 Pseudomonas
416	10.2	56.7	24	6	AX289618	Sequence	489	10.2	56.7	50	6	AX159966	AX159966 Sequence
417	10.2	56.7	24	6	AX291639	Sequence	490	10.2	56.7	14	6	E12333	E12333 Primer. 4/1
418	10.2	56.7	25	6	AR003574	Sequence	491	10.2	56.7	16	6	I33376	I33376 Sequence 34
419	10.2	56.7	25	6	AR075590	Sequence	492	10.2	56.7	17	6	AX356583	AX356583 Sequence
420	10.2	56.7	25	6	AR082293	Sequence	493	10.2	56.7	17	6	AX362565	AX362565 Sequence
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423	10.2	56.7	25	6	I78339	Sequence 13	496	10.2	56.7	19	6	AR069470	AR069470 Sequence
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430	10.2	56.7	27	6	AX287023	Sequence	503	10.2	56.7	20	6	AR203105	AR203105 Sequence

504	10	55.6	20	6	AR206607	AR206607 Sequence	c 577	10	55.6	31	6	AX249049	AX249049 Sequence
505	10	55.6	20	6	AR210698	AR210698 Sequence	c 578	10	55.6	32	6	A90735	A90735 Sequence
506	10	55.6	20	6	AX317881	AX317881 Sequence	c 579	10	55.6	32	6	AX288153	AX288153 Sequence
507	10	55.6	20	6	AX419559	AX419559 Sequence	c 580	10	55.6	32	6	AX339127	AX339127 Sequence
508	10	55.6	20	6	1233925	1233925 Sequence 27	c 581	10	55.6	33	6	A52073	A52073 Sequence
509	10	55.6	20	12	AB068545	AB068545 Synthetic	c 582	10	55.6	33	6	AR067682	AR067682 Sequence
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513	10	55.6	21	6	AX095342	AX095342 Sequence	c 586	10	55.6	33	10	MMTCRVJAL	222840 M. musculus
514	10	55.6	21	6	AX095353	AX095353 Sequence	c 587	10	55.6	35	6	AX008754	AX008754 Sequence
515	10	55.6	21	6	AX095407	AX095407 Sequence	c 588	10	55.6	35	6	AX192339	AX192339 Sequence
516	10	55.6	21	6	AX097158	AX097158 Sequence	c 589	10	55.6	35	6	BD000574	BD000574 Human pol
517	10	55.6	21	6	AX154443	AX154443 Sequence	c 590	10	55.6	36	6	AR068332	AR068332 Sequence
518	10	55.6	22	10	MMTC1902A	Z49042 M. musculus	c 591	10	55.6	36	6	AR178394	AR178394 Sequence
519	10	55.6	23	6	AR090535	AR090535 Sequence	c 592	10	55.6	36	6	AX260005	AX260005 Sequence
520	10	55.6	23	6	AR197570	AR197570 Sequence	c 593	10	55.6	36	6	AX220152	AX220152 Sequence
521	10	55.6	23	6	AX287628	AX287628 Sequence	c 594	10	55.6	39	6	AR031982	AR031982 Sequence
522	10	55.6	23	6	AX300573	AX300573 Sequence	c 595	10	55.6	40	6	AR062591	AR062591 Sequence
523	10	55.6	23	6	AX477190	AX477190 Sequence	c 596	10	55.6	40	6	AR206819	AR206819 Sequence
524	10	55.6	24	6	AR086083	AR086083 Sequence	c 597	10	55.6	40	6	AR206821	AR206821 Sequence
525	10	55.6	24	6	AR109796	AR109796 Sequence	c 598	10	55.6	40	6	AR206823	AR206823 Sequence
526	10	55.6	24	6	AR112021	AR112021 Sequence	c 599	10	55.6	40	6	115913	115913 Sequence 14
527	10	55.6	24	6	AR140437	AR140437 Sequence	c 600	10	55.6	40	6	196112	196112 Sequence 14
528	10	55.6	24	6	AR146918	AR146918 Sequence	c 601	10	55.6	41	6	AX327082	AX327082 Sequence
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533	10	55.6	25	6	122152	122152 Sequence 11	c 606	10	55.6	43	14	D88714	D88714 Hepatitis G
534	10	55.6	25	6	A91508	A101508 Sequence 35	c 607	10	55.6	43	14	D88720	D88720 Hepatitis G
535	10	55.6	25	6	AX042486	AX042486 Sequence	c 608	10	55.6	44	6	A13023	A13023 Partial HBV
536	10	55.6	25	6	AX476046	AX476046 Sequence	c 609	10	55.6	45	9	H55B3VB3	X84272 H. sapiens m
537	10	55.6	25	6	AX476047	AX476047 Sequence	c 610	10	55.6	45	9	H55B3VB3	765906 H. sapiens m
538	10	55.6	25	6	AX476048	AX476048 Sequence	c 611	10	55.6	45	9	H55B3VB3	765906 H. sapiens m
539	10	55.6	25	6	AX476049	AX476049 Sequence	c 612	10	55.6	48	6	AR011227	AR011227 Sequence
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543	10	55.6	25	6	AX476053	AX476053 Sequence	c 616	10	55.6	48	6	E16420	E16420 DNA encodin
544	10	55.6	25	10	MMTC11X42	Z49020 M. musculus	c 617	10	55.6	48	6	E16432	E16432 DNA encodin
545	10	55.6	26	6	AR142098	AR142098 Sequence	c 618	10	55.6	48	6	117865	117865 Sequence 95
546	10	55.6	26	6	AR151423	AR151423 Sequence	c 619	10	55.6	48	6	145981	145981 Sequence 5
547	10	55.6	26	6	AR157416	AR157416 Sequence	c 620	10	55.6	48	9	581442	581442 T cell anti
548	10	55.6	26	6	AX033900	AX033900 Sequence	c 621	10	55.6	49	6	AX026057	AX026057 Sequence
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550	10	55.6	26	6	AX049961	AX049961 Sequence	c 623	10	55.6	49	6	107176	107176 Sequence 3
551	10	55.6	26	6	AX374667	AX374667 Sequence	c 624	10	55.6	50	6	AR125775	AR125775 Sequence
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553	10	55.6	27	6	AR109730	AR109730 Sequence	c 626	10	55.6	50	6	AX199420	AX199420 Sequence
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556	10	55.6	27	10	MMM1314	X94907 M. musculus	c 629	10	55.6	50	6	147187	147187 Sequence 11
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558	10	55.6	28	6	AX098012	AX098012 Sequence	c 631	9.8	54.4	13	6	AX304729	AX304729 Sequence
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568	10	55.6	30	6	AR036161	AR036161 Sequence	c 641	9.8	54.4	17	6	AX215936	AX215936 Sequence
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570	10	55.6	30	6	AR125760	AR125760 Sequence	c 643	9.8	54.4	17	6	AX422860	AX422860 Sequence
571	10	55.6	30	6	AX192395	AX192395 Sequence	c 644	9.8	54.4	17	6	AX422861	AX422861 Sequence
572	10	55.6	30	6	BD000570	BD000570 Human pol	c 645	9.8	54.4	17	6	AX475064	AX475064 Sequence
573	10	55.6	30	6	100877	100877 Sequence 7	c 646	9.8	54.4	17	6	AX475065	AX475065 Sequence
574	10	55.6	30	6	104521	104521 Sequence 14	c 647	9.8	54.4	17	6	AX475066	AX475066 Sequence
575	10	55.6	30	6	147172	147172 Sequence 10	c 648	9.8	54.4	17	6	AX475067	AX475067 Sequence
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654	9.8	54.4	18	6	AR117374	AR117374 Sequence	727	9.8	54.4	25	6	AR137546	AR137546 Sequence
655	9.8	54.4	18	6	AR134127	AR134127 Sequence	728	9.8	54.4	25	6	AR139052	AR139052 Sequence
656	9.8	54.4	18	6	AR134128	AR134128 Sequence	729	9.8	54.4	25	6	AX042470	AX042470 Sequence
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658	9.8	54.4	18	6	AR190758	AR190758 Sequence	731	9.8	54.4	25	6	AX115810	AX115810 Sequence
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662	9.8	54.4	18	6	AX299455	AX299455 Sequence	735	9.8	54.4	25	6	AX476042	AX476042 Sequence
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665	9.8	54.4	19	6	AR035651	AR035651 Sequence	738	9.8	54.4	25	6	AX476045	AX476045 Sequence
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668	9.8	54.4	19	6	AR174299	AR174299 Sequence	741	9.8	54.4	26	6	AR208612	AR208612 Sequence
669	9.8	54.4	19	6	AR179745	AR179745 Sequence	742	9.8	54.4	26	6	AR037849	AR037849 Sequence
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674	9.8	54.4	19	6	AX304864	AX304864 Sequence	747	9.8	54.4	27	6	AR039462	AR039462 Sequence
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679	9.8	54.4	19	11	HUM265UYA	D50161 A PCR prime	752	9.8	54.4	27	6	AX058645	AX058645 Sequence
680	9.8	54.4	20	6	AR009309	AR009309 Sequence	753	9.8	54.4	27	6	AX117248	AX117248 Sequence
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683	9.8	54.4	20	6	AR095025	AR095025 Sequence	756	9.8	54.4	28	6	AR090426	AR090426 Sequence
684	9.8	54.4	20	6	AR136000	AR136000 Sequence	757	9.8	54.4	28	6	AR197461	AR197461 Sequence
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689	9.8	54.4	20	6	AX326875	AX326875 Sequence	762	9.8	54.4	30	6	AR030429	AR030429 Sequence
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695	9.8	54.4	21	6	A91533	A91533 Sequence 60	768	9.8	54.4	30	6	115727	115727 Sequence 2
696	9.8	54.4	21	6	A98267	A98267 Sequence 20	769	9.8	54.4	31	6	AR147746	AR147746 Sequence
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699	9.8	54.4	21	6	AX235879	AX235879 Sequence	772	9.8	54.4	31	6	AR195804	AR195804 Sequence
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705	9.8	54.4	23	6	A31977	A31977 Synthetic H	778	9.8	54.4	31	6	AX248132	AX248132 Sequence
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713	9.8	54.4	24	6	AR090844	AR090844 Sequence	786	9.8	54.4	32	6	AR208154	AR208154 Sequence
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C 799	9.8	54.4	36	6	A71933	Sequence 14	C 872	9.8	54.4	50	6	AX125773	Sequence
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C 801	9.8	54.4	36	6	AR042933	Sequence	C 874	9.8	54.4	50	6	AX165892	Sequence
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C 809	9.8	54.4	36	6	AX399404	Sequence 19	C 882	9.8	54.4	50	6	AX130256	Sequence
C 810	9.8	54.4	37	6	AX399405	Sequence 19	C 883	9.8	54.4	50	6	AX124941	Sequence
C 811	9.8	54.4	37	6	I75315	Sequence 7	C 884	9.8	54.4	50	6	AX258197	Sequence
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C 829	9.8	54.4	39	6	AX491657	Sequence	C 902	9.8	54.4	50	6	AX412019	Sequence
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C 834	9.8	54.4	40	6	AR031554	Sequence	C 907	9.8	54.4	50	6	AX412019	Sequence
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C 841	9.8	54.4	42	6	AR00577	Sequence	C 914	9.8	54.4	50	6	AX412019	Sequence
C 842	9.8	54.4	42	6	AR079771	Sequence	C 915	9.8	54.4	50	6	AX412019	Sequence
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C 848	9.8	54.4	42	12	S77087	Mus sp. T-C	C 921	9.8	54.4	50	6	AX412019	Sequence
C 849	9.8	54.4	43	6	E21666	Sequence 3	C 922	9.8	54.4	50	6	AX412019	Sequence
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955 9.6 53.3 25 6 AX038540
956 9.6 53.3 25 6 AX060480
957 9.6 53.3 25 6 BD005978
958 9.6 53.3 25 6 BD005985
959 9.6 53.3 25 6 BD005992
960 9.6 53.3 26 6 AX033455
961 9.6 53.3 26 6 AX365257
962 9.6 53.3 26 6 BD010752
963 9.6 53.3 26 6 E30993
964 9.6 53.3 27 6 A41158
965 9.6 53.3 27 6 AR030385
966 9.6 53.3 27 6 AR143813
967 9.6 53.3 27 6 AX203570
968 9.6 53.3 27 6 AX278552
969 9.6 53.3 27 6 AX280685
970 9.6 53.3 27 6 AX418361
971 9.6 53.3 27 6 AX418385
972 9.6 53.3 28 6 A40665
973 9.6 53.3 28 6 AR148899
974 9.6 53.3 28 6 AX031643
975 9.6 53.3 28 6 AX031913
976 9.6 53.3 28 6 AX032183
977 9.6 53.3 28 6 AX319390
978 9.6 53.3 29 6 A06418
979 9.6 53.3 29 6 A10237
980 9.6 53.3 29 6 A43384
981 9.6 53.3 29 6 AR035539
982 9.6 53.3 29 6 AR081876
983 9.6 53.3 29 6 AR093163
984 9.6 53.3 29 6 AX038844
985 9.6 53.3 29 6 AX440317
986 9.6 53.3 30 6 E11459
987 9.6 53.3 30 6 AR048682
988 9.6 53.3 30 6 AR093165
989 9.6 53.3 30 6 AR116796
990 9.6 53.3 30 6 AX058064
991 9.6 53.3 30 6 AX081615
992 9.6 53.3 31 6 AX374796
993 9.6 53.3 31 6 AX247988
994 9.6 53.3 31 6 AX249059
995 9.6 53.3 31 6 AX249195
996 9.6 53.3 31 6 AX249253
997 9.6 53.3 31 6 E11401
998 9.6 53.3 32 6 A43385
999 9.6 53.3 32 6 AR059492
1000 9.6 53.3 32 6 AR156441

ALIGNMENTS

RESULT 1
AX298039 18 bp
LOCUS AX298039 35 from Patent WO0183740.
DEFINITION AX298039
ACCESSION AX298039
VERSION AX298039.1 GI:17128125
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.

REFERENCE 1
artificial sequences.

AUTHORS Iversen, P. L. and Hudziak, R.

TITLE Splice-region antisense composition and method

JOURNAL Patent: WO 0183740-A 35 08-NOV-2001;

Avi Biopharma, Inc. (US)

FEATURES
source
1..18
Location/Qualifiers

BASE COUNT 3 a 6 c 7 g 2 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 18; DB 6; Length 18;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGGAAGCAGCTGGC 18

Db 1 CCCGGAAGCAGCTGGC 18

RESULT 2

AX298040 36 bp
LOCUS AX298040 36 from Patent WO0183740.
DEFINITION AX298040
ACCESSION AX298040
VERSION AX298040.1 GI:17128126

KEYWORDS

SOURCE synthetic construct.

ORGANISM synthetic construct

REFERENCE 1
artificial sequences.

AUTHORS Iversen, P. L. and Hudziak, R.

TITLE Splice-region antisense composition and method

JOURNAL Patent: WO 0183740-A 36 08-NOV-2001;

Avi Biopharma, Inc. (US)

FEATURES
source
1..36
Location/Qualifiers

BASE COUNT 6 a 11 c 12 g 7 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 18; DB 6; Length 36;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGGAAGCAGCTGGC 18

Db 17 CCCGGAAGCAGCTGGC 34

RESULT 3

I06689 28 bp
LOCUS I06689/c 28 from Patent WO 9009180.
DEFINITION I06689
ACCESSION I06689
VERSION I06689.1 GI:589476

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 28)

AUTHORS Smith, L.J. and A61K31.

TITLE METHODS AND COMPOSITIONS FOR TREATMENT OF CANCER USING

OLIGONUCLEOTIDES

JOURNAL Patent: WO 9009180-A 23-AUG-1990;

FEATURES
source
1..28
Location/Qualifiers
/organism="unknown"

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BASE COUNT      4 a      11 c      7 g      6 t
ORIGIN
Query Match      94.4%; Score 17; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 CCCGAGGAGCAGCTGCG 17
      17 CCCGAGGAGCAGCTGCG 1
Db      17 CCCGAGGAGCAGCTGCG 1

RESULT 4
LOCUS      AR003360
DEFINITION Sequence 7 from patent US 5744303.
ACCESSION  AR003360
VERSION     AR003360.1 GI:3964619
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 25)
AUTHORS    1990.R., Friend,S.H., Frebourg,T. and Ishioka,C.
TITLE      Functional assay for transcriptional regulator genes
JOURNAL    Patent: US 5744303-A 7 28-APR-1998;
FEATURES    Location/Qualifiers
            source          1..25
                        /organism="unknown"
BASE COUNT      4 a      8 c      7 g      6 t
ORIGIN
Query Match      83.3%; Score 15; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      4 GGAAGCAGCTGCG 18
      25 GGAAGCAGCTGCG 11
Db      25 GGAAGCAGCTGCG 11

RESULT 5
LOCUS      AX053071
DEFINITION Sequence 3 from Patent W00071078.
ACCESSION  AX053071
VERSION     AX053071.1 GI:12227129
KEYWORDS
SOURCE      synthetic construct.
ORGANISM    synthetic construct.
REFERENCE   1 (bases 1 to 26)
AUTHORS    Ehts,P. and Jund,R.
TITLE      Composition designed for implementing an antitumoral or antiviral
JOURNAL    Patent: WO 0071078-A 3 30-NOV-2000;
FEATURES    Location/Qualifiers
            source          1..26
                        /organism="synthetic construct"
                        /db_xref="taxon:32630"
                        /note="amorce"
BASE COUNT      5 a      9 c      7 g      5 t
ORIGIN
Query Match      82.2%; Score 14.8; DB 6; Length 26;
Best Local Similarity 88.9%; Pred. No. 2.9e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY      1 CCCGAGGAGCAGCTGCG 18
      22 CCCGAGGAGCAGCTGCG 5
Db      22 CCCGAGGAGCAGCTGCG 5

RESULT 6
LOCUS      AX464857
DEFINITION Sequence 8 from Patent W00212463.
ACCESSION  AX464857
VERSION     AX464857.1 GI:21899557
KEYWORDS
SOURCE      synthetic construct.
ORGANISM    synthetic construct.
REFERENCE   1
AUTHORS    Qualfetti,P., Mitchinson,C. and Ropp,T.H.
TITLE      Mutant EgII cellulase, DNA encoding such
JOURNAL    methods for obtaining same
            Patent: WO 0212463-A 8 14-FEB-2002;
            GENENCOR INTERNATIONAL, INC. (US)
FEATURES    Location/Qualifiers
            source          1..21
                        /organism="synthetic construct"
                        /db_xref="taxon:32630"
                        /note="primer"
BASE COUNT      3 a      8 c      7 g      3 t
ORIGIN
Query Match      73.3%; Score 13.2; DB 6; Length 21;
Best Local Similarity 83.3%; Pred. No. 1.9e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY      1 CCCGAGGAGCAGCTGCG 18
      4 CCTGGCAGGAGCAGCTGCG 21
Db      4 CCTGGCAGGAGCAGCTGCG 21

RESULT 7
LOCUS      AX464856
DEFINITION Sequence 7 from Patent W00212463.
ACCESSION  AX464856
VERSION     AX464856.1 GI:21899556
KEYWORDS
SOURCE      synthetic construct.
ORGANISM    synthetic construct.
REFERENCE   1
AUTHORS    Qualfetti,P., Mitchinson,C. and Ropp,T.H.
TITLE      Mutant EgII cellulase, DNA encoding such EgII compositions and
JOURNAL    methods for obtaining same
            Patent: WO 0212463-A 7 14-FEB-2002;
            GENENCOR INTERNATIONAL, INC. (US)
FEATURES    Location/Qualifiers
            source          1..27
                        /organism="synthetic construct"
                        /db_xref="taxon:32630"
                        /note="primer"
BASE COUNT      3 a      10 c      11 g      3 t
ORIGIN
Query Match      73.3%; Score 13.2; DB 6; Length 27;
Best Local Similarity 83.3%; Pred. No. 1.7e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY      1 CCCGAGGAGCAGCTGCG 18
      21 CCTGGCAGGAGCAGCTGCG 4
Db      21 CCTGGCAGGAGCAGCTGCG 4

RESULT 8
LOCUS      AR137946
DEFINITION Sequence 22 from patent US 6197580.
ACCESSION  AR137946
VERSION     AR137946.1 GI:14479455
```

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Susulic,V.S. and Duzic,E.
TITLE Transcriptional regulation of the human .beta.3-adrenergic receptor gene
JOURNAL Patent: US 6197580-A 22 06-MAR-2001;
FEATURES Location/Qualifiers
source 1..26
BASE COUNT 3 a 11 c 5 g 7 t
ORIGIN

Query Match 68.9%; Score 12.4; DB 6; Length 26;
Best Local Similarity 92.9%; Pred. No. 4.3e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 GAAGCAGCTGTGGC 18
DB 24 GAAGCAGCTGTGGC 11

RESULT 9
LOCUS AX348011/c 17 bp DNA linear PAT 06-PEB-2002
DEFINITION Sequence 44 from Patent EP1172444.
ACCESSION AX348011
VERSION AX348011.1 GI:18614121
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Schreiber,S., Hampe,J. and Mascheretti,S.
TITLE Diagnostic use of polymorphisms in the gene coding for the tnfr receptor II and method for detecting non-responders to anti-tnfr therapy
JOURNAL Patent: EP 1172444-A 44 16-JAN-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Reverse Primer"
BASE COUNT 3 a 8 c 4 g 2 t
ORIGIN

Query Match 67.8%; Score 12.2; DB 6; Length 17;
Best Local Similarity 82.4%; Pred. No. 6.1e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CCGGAGGCGCTGTGG 17
DB 17 CCGGAGGCGCTGTGG 1

RESULT 10
LOCUS AR174377/c 20 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 37 from patent US 6306555.
ACCESSION AR174377
VERSION AR174377.1 GI:17914697
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P., Butler,M.M. and Wyatt,J.
TITLE Antisense inhibition of C/EBP alpha expression
JOURNAL Patent: US 6306555-A 37 23-OCT-2001;
FEATURES Location/Qualifiers

source 1..20
BASE COUNT 3 a 8 c 6 g 3 t
ORIGIN

Query Match 67.8%; Score 12.2; DB 6; Length 20;
Best Local Similarity 82.4%; Pred. No. 5.8e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CCGGAGGCGCTGTGG 17
DB 17 CCGGAGGCGCTGTGG 1

RESULT 11
LOCUS E10818 23 bp DNA linear PAT 29-SEP-1997
DEFINITION FITC labeling sequencing primer for detecting cellulose from Humicola insolens.
ACCESSION E10818
VERSION E10818.1 GI:22027913
KEYWORDS JP 1996056663-A/8.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 23)
AUTHORS Watanabe,M., Sumida,N., Kawabata,K., Aoyanagi,K., Hamaya,T., Hirayama,M. and Murakami,T.
TITLE NEW CELLULOSE AND ITS GENE
JOURNAL Patent: JP 1996056663-A 8 05-MAR-1996;
COMMENT MEIJI SEIKA KAISHA LTD
OS None
OC Artificial sequences.
PN JP 1996056663-A/8
PD 05-MAR-1996
PE 29-AUG-1994 JP 1994203564
PI WATANABE MANABU, SUMIDA NAOMI, KAWABATA KEIKO, AOYANAGI KAORU, HAMAYA TORU, HIRAYAMA MASAO, MURAKAMI TAKESHI PC
C12N9/42.C12N15/09.(C12N9/42.C12R1:19);
CC strandedness: Single;
CC topology: linear;
CC hypothetical: No;
FH key Location/Qualifiers
FT source 1..23
FT /organism="Artificial sequences" FT
misc_feature 1..23 /note="Primer,WATA-11",
FEATURES Location/Qualifiers
source 1..23
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 6 a 5 c 8 g 4 t
ORIGIN

Query Match 67.8%; Score 12.2; DB 6; Length 23;
Best Local Similarity 82.4%; Pred. No. 5.6e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 CCGGAGGCGCTGTGGC 18
DB 3 CCGGAGGCGCTGTGGC 19

RESULT 12
LOCUS AR066373 26 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 12 from patent US 5849994.
ACCESSION AR066373
VERSION AR066373.1 GI:5996589
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

OY 1 CCCGAGGAGCTCTGG 17
||| ||||| |||||
Db 30 CCCACAGGAGCTCTGG 46

RESULT 17
AX384794/c AX384794 22 bp DNA linear PAT 19-MAR-2002
LOCUS AX384794
DEFINITION Sequence 12 from Patent WO0191548.
ACCESSION AX384794
VERSION AX384794.1 GI:19577929
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Roberds, S.L. and Huff, R.M.
TITLE Mice heterozygous for wfs1 gene as mouse models for depression
JOURNAL Patent: WO 0191548-A 12 06-DEC-2001;
PHARMACIA & UPJOHN COMPANY (US)
FEATURES
source 1..22
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Primer"

BASE COUNT 3 a 8 c 6 g 5 t
ORIGIN

Query Match 66.7%; Score 12; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AAGCGAGTCTGG 17
||||| ||||| |||||
Db 21 AAGCGAGTCTGG 10

RESULT 18
AR095087/c AR095087 23 bp DNA linear PAT 08-SEP-2000
LOCUS AR095087
DEFINITION Sequence 2 from patent US 6002066.
ACCESSION AR095087
VERSION AR095087.1 GI:10022625
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Leung, W.-P., Karlsson, L., Zhou, L. and Peterson, P.A.
TITLE H2-M modified transgenic mice
JOURNAL Patent: US 6002066-A 2 14-DEC-1999;
FEATURES
source 1..23
Location/Qualifiers
BASE COUNT 5 a 8 c 5 g 5 t
ORIGIN

Query Match 66.7%; Score 12; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 7e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AAGCGAGTCTGG 17
||||| ||||| |||||
Db 23 AAGCGAGTCTGG 12

RESULT 19
AX447459/c AX447459 24 bp DNA linear PAT 03-JUL-2002
LOCUS AX447459
DEFINITION Sequence 3914 from Patent WO0216649.
ACCESSION AX447459
VERSION AX447459.1 GI:21696358

KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Gunderson, K.
TITLE Probes and decoder oligonucleotides
JOURNAL Patent: WO 0216649-A 3914 28-FEB-2002;
ILLUMINA, INC. (US)
FEATURES
source 1..24
Location/Qualifiers
BASE COUNT 5 a 7 c 5 g 7 t
ORIGIN

Query Match 66.7%; Score 12; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.9e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 CGGAGGAGCTC 14
||||| ||||| |||||
Db 19 CGGAGGAGCTC 8

RESULT 20
AR108592/c AR108592 26 bp DNA linear PAT 14-FEB-2001
LOCUS AR108592
DEFINITION Sequence 1 from patent US 6110902.
ACCESSION AR108592
VERSION AR108592.1 GI:12824079
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Mohler, H. and Bolson, D.
TITLE Method for the inhibition of neuronal activity leading to a focal
JOURNAL Patent: US 6110902-A 1 29-AUG-2000;
FEATURES
source 1..26
Location/Qualifiers
BASE COUNT 7 a 7 c 7 g 5 t
ORIGIN

Query Match 66.7%; Score 12; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.8e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AAGCGAGTCTGG 17
||||| ||||| |||||
Db 17 AAGCGAGTCTGG 6

RESULT 21
AX092972/c AX092972 26 bp DNA linear PAT 30-MAR-2001
LOCUS AX092972
DEFINITION Sequence 31 from Patent WO0118225.
ACCESSION AX092972
VERSION AX092972.1 GI:13509457
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 26)
AUTHORS Zhang, N.
TITLE Targeting constructs and transgenic animals produced therewith
JOURNAL Patent: WO 0118225-A 31 15-MAR-2001;
Xenogen Corporation (US)
FEATURES
source 1..26
Location/Qualifiers

BASE COUNT	6 a	9 c	7 g	4 t	
ORIGIN	/organism="synthetic construct" /db_xref="taxon:32630" /note="primer R51"				
Query Match	66.7%; Score 12; DB 6; Length 26;				
Best Local Similarity	100.0%; Pred. No. 6.8e+05;				
Matches 12; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
OY	6 AAGCAGCTCTGG	17			
Db	12 AAGCAGCTCTGG	1			
RESULT 22					
LOCUS	BD012014	26 bp	DNA	linear	PAT 02-JAN-2002
DEFINITION	Hydrocephalus model animal.				
ACCESSION	BD012014	1 GI:22092203			
VERSION	MO 0101767-A/4.				
KEYWORDS	synthetic construct.				
SOURCE	artificial sequences.				
ORGANISM	1 (bases 1 to 26)				
REFERENCE	Sakakibara,S., Noda,T. and Okano,H.				
AUTHORS	Hydrocephalus model animal				
TITLE	Patent: JP 2001017027-A 4 23-JAN-2001;				
JOURNAL	SCIENCE & TECH AGENCY				
OS	Artificial Sequence				
COMMENT	PN JP 2001017027-A/4				
BASE COUNT	6 a	8 c	7 g	5 t	
ORIGIN	/organism="synthetic construct" /db_xref="taxon:32630"				
Query Match	66.7%; Score 12; DB 6; Length 26;				
Best Local Similarity	100.0%; Pred. No. 6.8e+05;				
Matches 12; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
OY	6 AAGCAGCTCTGG	17			
Db	13 AAGCAGCTCTGG	2			
RESULT 23					
LOCUS	ES5063	26 bp	DNA	linear	PAT 31-JAN-2002
DEFINITION	Hydrocephalic model animal.				
ACCESSION	ES5063.1	GI:18629732			
VERSION	JP 2001017027-A/4.				
KEYWORDS	synthetic construct.				
SOURCE	artificial sequences.				
ORGANISM	1 (bases 1 to 26)				
REFERENCE	Sakakibara,S., Noda,T. and Okano,H.				
AUTHORS	Hydrocephalus model animal				
TITLE	Patent: JP 2001017027-A 4 23-JAN-2001;				
JOURNAL	SCIENCE & TECH AGENCY				
OS	Artificial Sequence				
COMMENT	PN JP 2001017027-A/4				

Query Match 66.7%; Score 12; DB 23; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.8e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AAGCAGCTCTGG 17
|||||
DB 13 AAGCAGCTCTGG 2

RESULT 25
BD012788/c
LOCUS BD012788 28 bp DNA linear PAT 02-AUG-2002
DEFINITION An animal with a knocked out alpha-tocopherol transfer protein gene.
ACCESSION BD012788
VERSION BD012788.1 GI:22092977
KEYWORDS WO 0113716-A/3.
SOURCE synthetic construct.
ORGANISM artificial construct.
REFERENCE 1 (bases 1 to 28)
AUTHORS Inoue, K., Arai, H., Arita, M., Jishage, K. and Suzuki, H.
TITLE An animal with a knocked out alpha-tocopherol transfer protein gene
JOURNAL Patent: WO 0113716-A 3 01-MAR-2001;
KEIZO INOUE, HIROYUKI ARAI, MAKOTO ARITA, KOICHI JISHAGE, IROSHI SUZUKI
OS Artificial Sequence
COMMENT PN WO 0113716-A/3
PD 01-MAR-2001
PF 24-AUG-2000 WO 2000JP005686
PR 24-AUG-1999 JP 99P 237003
PI KEIZO INOUE, HIROYUKI ARAI, MAKOTO ARITA, KOICHI JISHAGE, PI HIROSHI SUZUKI
PC A01K67/027, C12N15/12, C12N5/06, C12N5/16, A61K45/00, A61P3/02, PC A61P9/10.
PP A61P3/10, G01N33/50, G01N33/15
CC
XX

FEATURES
source 1..28 Location/Qualifiers.
FH Key Location/Qualifiers.
BASE COUNT 6 a 9 c 7 g 6 t
ORIGIN

Query Match 66.7%; Score 12; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AAGCAGCTCTGG 17
|||||
DB 27 AAGCAGCTCTGG 16

RESULT 26
BD008223/c
ID BD008223 standard; DNA; SYN: 28 BP.
AC BD008223;
XX
XX BD008223.1
SV
XX
XX 08-FEB-2002 (Rel. 70, Created)
DT 08-FEB-2002 (Rel. 70, Last updated, Version 1)
XX
DE An animal with a knocked out alpha-tocopherol transfer protein gene.
XX JP 03075485-T/3.
KW
XX
XX synthetic construct
OC artificial sequence.
XX
RN [1]

RP 1-28
RA Inoue K., Arai H., Arita M., Jishage K., Suzuki H.;
RT "An animal with a knocked out alpha-tocopherol transfer protein gene";
RL Patent number JP03075485-T/3, 23-FEB-2001
RL KEIZO INOUE, HIROYUKI ARAI, MAKOTO ARITA, KOICHI JISHAGE, IROSHI SUZUKI.
XX
XX
OS Artificial Sequence
CC PN JP 03075485-T/3
CC PD 23-FEB-2001
CC PF 24-AUG-2000 JP 2000005686
CC PR 24-AUG-1999 JP 99P 237003
CC PI KEIZO INOUE, HIROYUKI ARAI, MAKOTO ARITA, KOICHI JISHAGE,
CC PT HIROSHI SUZUKI
CC PC A01K67/027, C12N15/12, C12N5/06, C12N5/16, A61K45/00, A61P3/02,
CC PC A61P9/10,
CC PC A61P3/10, G01N33/50, G01N33/15
CC
CC
CC FH Key Location/Qualifiers
CC FT source 1..28
CC FT source /organism="Artificial Sequence"
XX
XX
FH Key Location/Qualifiers
FH source 1..28
FT /db_xref="taxon:32630"
FT /organism="synthetic construct"
XX
XX
SQ Sequence 28 BP; 6 A; 9 C; 7 G; 6 T; 0 other;

Query Match 66.7%; Score 12; DB 23; Length 28;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AAGCAGCTCTGG 17
|||||
DB 27 AAGCAGCTCTGG 16

RESULT 27
AX327013/c
LOCUS AX327013 20 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 209 from Patent WO017894.
ACCESSION AX327013
VERSION AX327013.1 GI:18097724
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Keith, T.
TITLE Novel human gene relating to respiratory diseases, obesity, and inflammatory bowel disease
JOURNAL Patent: WO 0178894-A 209 25-OCT-2001;
Genome Therapeutics Corp. (US)
FEATURES
source 1..20 Location/Qualifiers
FH Key Location/Qualifiers
BASE COUNT 5 a 5 c 5 g 5 t
ORIGIN

Query Match 65.6%; Score 11.8; DB 6; Length 20;
Best Local Similarity 86.7%; Pred. No. 9.2e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CCGGAGGCACTCT 15
|||||
DB 15 CCTGAGGCACTCT 1
CCTGAGGCACTCT 1

RESULT 28
I32023/c

LOCUS 132023 21 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 34 from patent US 5585232.
ACCESSION 132023
VERSION 132023.1 GI:1822814
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Fair,S.B.
TITLE Methods and diagnostic kits for determining toxicity utilizing E.
JOURNAL coli stress promoters fused to reporter genes
FEATURES
source Location/Qualifiers
BASE COUNT 4 a 8 c 5 g 4 t
ORIGIN
Query Match 65.6%; Score 11.8; DB 6; Length 21;
Best Local Similarity 86.7%; Pred. No. 9e+05; Mismatches 2; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 CCGGAGGCGACTCT 15
Db 19 CCGGAGGCGGTTT 5
RESULT 29
LOCUS 132707 21 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 34 from patent US 5589337.
ACCESSION 132707
VERSION 132707.1 GI:1823498
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Fair,S.B.
TITLE Methods and diagnostic kits for determining toxicity utilizing
JOURNAL bacterial stress promoters fused to reporter genes
FEATURES
source Location/Qualifiers
BASE COUNT 4 a 8 c 5 g 4 t
ORIGIN
Query Match 65.6%; Score 11.8; DB 6; Length 21;
Best Local Similarity 86.7%; Pred. No. 9e+05; Mismatches 2; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 CCGGAGGCGACTCT 15
Db 19 CCGGAGGCGGTTT 5
RESULT 30
LOCUS AY082157 23 bp DNA linear PAT 27-FEB-2001
DEFINITION Sequence 7 from Patent WO0109293.
ACCESSION AY082157
VERSION AY082157.1 GI:13170957
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 23)
AUTHORS Sheppard,P.O., Baird,N. and Bishop,P.D.
TITLE Mammalian adhesion protease peptides
JOURNAL Patent: WO 0109293-A 7 08-FEB-2001;
ZymoGenetics, Inc. (US)

FEATURES
source Location/Qualifiers
BASE COUNT 5 a 6 c 6 g 6 t
ORIGIN
Query Match 65.6%; Score 11.8; DB 6; Length 23;
Best Local Similarity 86.7%; Pred. No. 8.8e+05; Mismatches 2; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 CCGGAGGCGACTCT 15
Db 7 CCGGAGGCGACTCT 21
RESULT 31
LOCUS AR198876 24 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 178 from patent US 6355411.
ACCESSION AR198876
VERSION AR198876.1 GI:20248950
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Ausubel,F., Goodman,H.M., Rahne,L.G., Mahajan-Miklos,S., Tan,M.-W.,
TITLE Cao,H., Drenthard,E. and Tsongalis,J.
JOURNAL virulence-associated nucleic acid sequences and uses thereof
FEATURES
source Location/Qualifiers
BASE COUNT 5 a 7 c 9 g 3 t
ORIGIN
Query Match 65.6%; Score 11.8; DB 6; Length 24;
Best Local Similarity 86.7%; Pred. No. 8.7e+05; Mismatches 2; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 2 CCGGAGGCGACTCTG 16
Db 9 CCGGAGGCGAGCTG 23
RESULT 32
LOCUS AX428028 25 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 5 from Patent WO0233105.
ACCESSION AX428028
VERSION AX428028.1 GI:21538077
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Creissen,G.P. and Mullineaux,P.M.
TITLE Methods and means for modification of plant characteristics
JOURNAL Patent: WO 0233105-A 5 25-APR-2002;
PLANT BIOSCIENCE LTD (GB)
FEATURES
source Location/Qualifiers
BASE COUNT 4 a 5 c 9 g 7 t
ORIGIN
Query Match 65.6%; Score 11.8; DB 6; Length 25;
Best Local Similarity 86.7%; Pred. No. 8.6e+05; Mismatches 2; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CCCGAGAGCACTCT 15
|||||
DB 8 CCCGAGAGCGGTTT 22

RESULT 33
LOCUS A05131 45 bp DNA linear PAT 04-MAY-1993
DEFINITION Oligonucleotide 19 for bovine growth hormone.
ACCESSION A05131
VERSION A05131.1 GI:345018

KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
FEATURES
Source Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT 9 a 14 c 9 g 13 t
ORIGIN

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Best Local Similarity 86.7%; Pred. No. 7.3e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 GGAGGAGCTGGC 18
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DB 20 GGAGGCACTCTGGC 6

RESULT 34
LOCUS AX201806 22 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 15 from Patent W00153537.
ACCESSION AX201806
VERSION AX201806.1 GI:15391652

KEYWORDS
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 22)
AUTHORS Moskowitz,D.W.
TITLE Nitric oxide synthase gene diagnostic polymorphisms
JOURNAL Patent: WO 0153537-A 15 26-JUN-2001;

FEATURES
Source Location/Qualifiers
1..22
/organism="Homo sapiens"
/db_xref="taxon:9606"

misc_feature
1..22
/note="STAR_1 (Se-Cys tRNA gene transcription activating factor)"
BASE COUNT 6 a 9 c 4 g 3 t
ORIGIN

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Best Local Similarity 77.8%; Pred. No. 1.1e+06;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CCCGAGAGCACTGGC 18
|||||
DB 5 CCCAGATGCACTGGC 22

RESULT 35
LOCUS E04526 25 bp DNA linear PAT 29-SEP-1997
DEFINITION PCR primer.
ACCESSION E04526
VERSION E04526.1 GI:2172727

KEYWORDS JP 1993078397-A/1.
SOURCE synthetic construct.
ORGANISM synthetic construct
FEATURES
Source Location/Qualifiers
1..25
/organism="synthetic construct"
/db_xref="taxon:32630"

REFERENCE 1 (bases 1 to 25)
AUTHORS Yamazaki,C., Takasu,N., Negoro,T. and Agui,H.
TITLE THROMBOLYTIC PROTEIN
JOURNAL Patent: JP 1993078397-A 1 30-MAR-1993;
SUMITOMO PHARMACEUT CO LTD

COMMENT
OS Artificial gene
OC Artificial sequence; Genes.
PN JP 1993078397-A/1
PD 30-MAR-1993
PF 29-JAN-1991 JP 1991029624
PI YAMAZAKI CHIE, TAKASU NOKO, NEGORO TAKASU, AGUI HIRO PC
C07K13/00,A61K37/24,A61K37/54,C12N1/19,C12N1/21,C12N5/10, PC
C12N9/64,
PC C12N15/58,C12N15/62,C12N15/70,C12N15/81,C12N15/85//C12P21/02,
PC (C12N1/21,
PC C12R1:19),(C12P21/02,C12R1:19);
CC strandedness: Single;
CC topology: linear.

BASE COUNT 3 a 10 c 9 g 3 t
ORIGIN

Query Match 64.4%; Score 11.6; DB 6; Length 25;
Best Local Similarity 77.8%; Pred. No. 1.1e+06;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CCCGAGAGCACTGGC 18
|||||
DB 2 CCTGAGAGCAGCGGC 19

RESULT 36
LOCUS ARI43851 27 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 113 from patent US 6205404.
ACCESSION ARI43851
VERSION ARI43851.1 GI:15105137

KEYWORDS
SOURCE unknown.

ORGANISM unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Michaels,G.S., Mikelisaar,R.-H. and Feldmann,R.J.
TITLE DNA-binding proteins of the zinc-finger class
JOURNAL Patent: US 6205404-A 113 20-MAR-2001;

FEATURES
Source Location/Qualifiers
1..27
/organism="unknown"
BASE COUNT 8 a 7 c 10 g 2 t
ORIGIN

Query Match 64.4%; Score 11.6; DB 6; Length 27;
Best Local Similarity 77.8%; Pred. No. 1.1e+06;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CCCGAGAGCACTGGC 18
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DB 1 CCAGAGAGCGCCTGGC 18

RESULT 37
LOCUS AX248747 31 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 826 from Patent W00166800.
ACCESSION AX248747
VERSION AX248747.1 GI:15863370

KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Hardin,S.H., Briggs,J.M., Tu,S.C., Gao,X. and Willson,R.
TITLE Real-time sequence determination
JOURNAL Patent: WO 0204680-A 17 JAN-2002;
VISIGEN Biotechnologies, Inc. (US)
FEATURES
source
1. .33
/organism="Homo sapiens"
/db_xref="taxon:9606"

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ORIGIN

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Best Local Similarity 77.8%; Pred. No. 1e+06;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCCGGAAGCAGCTGTGCC 18
Db 12 CCTTAAAGCGCGGTGCC 29

RESULT 38
AX399412 33 bp DNA linear PAT 28-MAY-2002
LOCUS
DEFINITION Sequence 16 from Patent WO204680.
ACCESSION AX399412
VERSION AX399412.1 GI:21261983
KEYWORDS
ORGANISM Thermus aquaticus.
Thermus aquaticus
Bacteria; Thermus/Delnococcus group; Delnococci; Thermales;
Thermaceae; Thermus.

REFERENCE
AUTHORS Hardin,S.H., Briggs,J.M., Tu,S.C., Gao,X. and Willson,R.
TITLE Real-time sequence determination
JOURNAL Patent: WO 0204680-A 16 JAN-2002;
VISIGEN Biotechnologies, Inc. (US)
FEATURES
source
1. .33
/organism="Thermus aquaticus"
/db_xref="taxon:271"

variation
16. .18
/note="Tag Pol I Mutation: AA 655 asp to cys: codon: gac
-> tgc"

BASE COUNT 2 a 14 c 13 g 4 t
ORIGIN

Query Match 64.4%; Score 11.6; DB 6; Length 33;
Best Local Similarity 77.8%; Pred. No. 1e+06;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCCGGAAGCAGCTGTGCC 18
Db 2 CCCGGAAGCGCGGTGCC 19

RESULT 39
AX399413 33 bp DNA linear PAT 28-MAY-2002
LOCUS
DEFINITION Sequence 17 from Patent WO204680.
ACCESSION AX399413
VERSION AX399413.1 GI:21261984
KEYWORDS
ORGANISM Thermus aquaticus.
Thermus aquaticus
Bacteria; Thermus/Delnococcus group; Delnococci; Thermales;
Thermaceae; Thermus.

REFERENCE
1

AUTHORS Hardin,S.H., Briggs,J.M., Tu,S.C., Gao,X. and Willson,R.
TITLE Real-time sequence determination
JOURNAL Patent: WO 0204680-A 17 JAN-2002;
VISIGEN Biotechnologies, Inc. (US)
FEATURES
source
1. .33
/organism="Thermus aquaticus"
/db_xref="taxon:271"

variation
16. .18
/note="Tag Pol I Mutation Complimentary Strand: AA 516
655 asp to cys: antisense codon: gtc -> gca. 5' to 3'
listing."

BASE COUNT 4 a 13 c 14 g 2 t
ORIGIN

Query Match 64.4%; Score 11.6; DB 6; Length 33;
Best Local Similarity 77.8%; Pred. No. 1e+06;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCCGGAAGCAGCTGTGCC 18
Db 32 CCCGGAAGCGCGGTGCC 15

RESULT 40
AX297519 44 bp DNA linear PAT 21-NOV-2001
LOCUS
DEFINITION Sequence 9281 from Patent WO0179548.
ACCESSION AX297519
VERSION AX297519.1 GI:17059210
KEYWORDS
ORGANISM synthetic construct.
synthetic construct
artificial sequences.

REFERENCE
AUTHORS Barany,F., Zivrl,M., Gerry,N.P., Favis,R. and Kilman,R.
TITLE Method of designing addressable array for detection of nucleic acid
sequence differences using ligase detection reaction
JOURNAL Patent: WO 0179548-A 9281 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
source
1. .44
/organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT 11 a 11 c 15 g 7 t
ORIGIN

Query Match 64.4%; Score 11.6; DB 6; Length 44;
Best Local Similarity 77.8%; Pred. No. 9.2e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCCGGAAGCAGCTGTGCC 18
Db 20 CCCGTAAGCCCGTATGCC 37

Search completed: December 2, 2002, 13:33:44
Job time : 2679 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 2, 2002, 12:36:58 ; Search time 252 Seconds

(without alignments)
160.857 Million cell updates/sec

Title: US-09-848-868-35

Sequence: 1 cccggaagcagctcgc 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	24	AA519106 Human p53 coding s
2	18	100.0	36	24	AA519107 Human p53 coding s
3	18	100.0	37	20	AA265511 WO 9909191 Segid #
4	15	83.3	25	15	AA061823 Primer for mutant
5	14.8	82.2	26	22	AA061823 PCR primer used to
6	13.2	73.3	21	24	AA142029 T. reesei endogluc
7	13.2	73.3	27	24	AA142028 T. reesei endogluc
8	12.8	71.1	18	17	AA150605 Human CERP hairpin
9	12.8	71.1	18	17	AA150701 Rabbit CERP hairpin

C	10	12.8	71.1	28	16	AA092447	CD3 delta chain 3'
C	11	12.8	71.1	30	11	AA060664	N-terminus probe u
C	12	12.4	68.9	18	17	AA150604	Human CERP hairpin
C	13	12.4	68.9	18	17	AA150700	Rabbit CERP hairpin
C	14	12.4	68.9	26	21	AA087923	Human beta-3-adren
C	15	12.2	67.8	17	24	ABK33460	Human TNF-receptor
C	16	12.2	67.8	20	14	AA050876	HSV2 primer. Synt
C	17	12.2	67.8	20	14	AA050876	PCR primer. Synt
C	18	12.2	67.8	20	24	AA155599	PCR primer #5 used
C	19	12.2	67.8	20	24	AB042225	Human/mouse C/EBP
C	20	12.2	67.8	26	20	AA089817	Human calicron 1
C	21	12.2	67.8	26	20	AA089817	PCR primer for SV
C	22	12.2	67.8	32	16	AA087560	HTLVIII amplifica
C	23	12.2	67.8	32	16	AA089758	Primer XHOM to amp
C	24	12.2	67.8	36	21	AA111413	Oligo for mutatin
C	25	12.2	67.8	36	21	AA074925	Nucleotide sequenc
C	26	12.2	67.8	46	21	AA074926	Nucleotide sequenc
C	27	12.2	67.8	50	22	AA127830	Nucleotide sequenc
C	28	12.2	67.8	50	22	AA088378	Human SNP oligonuc
C	29	12.2	67.8	50	22	AA088378	Pig PRCpx 3' UTR o
C	30	12.2	67.8	50	22	AA088378	Wolfram Syndrome 1
C	31	12.2	67.8	23	19	AAV41645	Oligonucleotide ad
C	32	12.2	67.8	24	24	AA039607	ADA knock-out spec
C	33	12.2	67.8	26	20	AA009063	PKR-LR-VN/VEGF 5' tr
C	34	12.2	67.8	26	22	AA010772	Mouse Musashi 1 PC
C	35	12.2	67.8	28	22	AA062210	PCR primer for PKG
C	36	12.2	67.8	28	24	AB0703702	Human Neurogenin-3
C	37	12.2	67.8	47	21	AA065981	Human map-related
C	38	12.2	67.8	15	18	AA076214	Human IL-4 receptor
C	39	11.8	65.6	15	20	AA054609	Human IL-4 receptor
C	40	11.8	65.6	15	21	AA019575	Human IL4 receptor
C	41	11.8	65.6	15	21	AA033453	Low adenosine anti
C	42	11.8	65.6	15	22	AA049083	IGF-I oligonucleot
C	43	11.8	65.6	15	22	AA052897	IGF-I oligonucleot
C	44	11.8	65.6	17	24	ABN01478	Human GDMLP-1 17-m
C	45	11.8	65.6	17	24	ABN01478	Human GDMLP-1 17-m
C	46	11.8	65.6	17	24	ABN01480	Human GDMLP-1 17-m
C	47	11.8	65.6	20	21	AA082974	Human IGF-1 antis
C	48	11.8	65.6	20	21	AA082974	gsh-lacZ fusion co
C	49	11.8	65.6	20	15	AA054942	Enzymatic primer R3
C	50	11.8	65.6	21	20	AA074050	Enzymatic primer R3
C	51	11.8	65.6	21	20	AA074050	Primer used to amp
C	52	11.8	65.6	23	20	AA085519	Glutathione synth
C	53	11.8	65.6	24	20	AA085519	Human GDMLP-1 25-m
C	54	11.8	65.6	25	24	ABN04407	Human GDMLP-1 25-m
C	55	11.8	65.6	25	24	ABN04408	Human GDMLP-1 25-m
C	56	11.8	65.6	25	24	ABN04409	Human GDMLP-1 25-m
C	57	11.8	65.6	25	24	ABN04410	Human GDMLP-1 25-m
C	58	11.8	65.6	25	24	ABN04411	Human GDMLP-1 25-m
C	59	11.8	65.6	25	24	ABN04412	Human GDMLP-1 25-m
C	60	11.8	65.6	25	24	ABN04413	Human GDMLP-1 25-m
C	61	11.8	65.6	25	24	ABN04414	Human GDMLP-1 25-m
C	62	11.8	65.6	25	24	ABN04415	Human GDMLP-1 25-m
C	63	11.8	65.6	25	24	ABN04416	Human GDMLP-1 25-m
C	64	11.8	65.6	25	24	ABN04417	Human GDMLP-1 25-m
C	65	11.8	65.6	25	24	ABN04418	Human GDMLP-1 25-m
C	66	11.8	65.6	33	22	AA062818	DpnI endonuclease
C	67	11.8	65.6	40	18	AA048227	PCR primer used fo
C	68	11.8	65.6	41	21	AA015263	PCR primer for a m
C	69	11.8	65.6	41	21	AA015264	Human map-related
C	70	11.8	65.6	47	21	AA068926	PCR primer for a m
C	71	11.8	65.6	49	21	AA015278	Human SNP oligonuc
C	72	11.8	65.6	50	22	AA029107	Primer used in rec
C	73	11.8	65.6	50	22	AA029107	Nitric oxide synth
C	74	11.6	64.4	22	14	AA023166	Caenorhabditis ele
C	75	11.6	64.4	25	14	AA041194	Human foetal liver
C	76	11.6	64.4	27	20	AA027139	Type C lectin PCR
C	77	11.6	64.4	29	18	AA020189	Human single nucle
C	78	11.6	64.4	31	22	AA092450	DNA polymerase I f
C	79	11.6	64.4	33	24	ABK40144	Coagulation factor
C	80	11.6	64.4	33	24	ABK40145	
C	81	11.6	64.4	33	24	ABK40145	
C	82	11.6	64.4	40	24	ABN88587	

83	11.6	64.4	44	24	ABI82087	K-ras mutation det	c 156	11.2	62.2	26	20	AAV72127	Human catalytic te
c 84	11.6	64.4	45	22	AA564186	Human prostate cdn	c 157	11.2	62.2	27	17	AAI1697	5' primer for yeas
c 85	11.6	64.4	48	20	AA210910	Probe #2 for adeny	c 158	11.2	62.2	27	23	AAH8704	Human procollagen
c 86	11.6	64.4	50	22	AAI29297	Human SNP oligonuc	c 159	11.2	62.2	27	24	AA517030	Yeast cyclohexamid
c 87	11.6	64.4	50	22	AAI23396	Human SNP oligonuc	c 160	11.2	62.2	28	15	AAO67014	Endoglucanase type
c 88	11.6	64.4	50	22	AAI32397	Human SNP oligonuc	c 161	11.2	62.2	28	20	AAV82714	Partial sequence o
c 89	11.6	64.4	50	22	AAI34260	Human SNP oligonuc	c 162	11.2	62.2	28	21	AAV6314	Xyloglucan endoglu
c 90	11.6	64.4	50	22	AAI34540	Human SNP oligonuc	c 163	11.2	62.2	28	21	AAV89549	Xyloglucan endoglu
c 91	11.6	63.3	50	22	AAI75365	Human silent SNP c	c 164	11.2	62.2	28	22	AA502157	Partial DNA #7 enc
c 92	11.4	63.3	20	24	AAI43513	Human DBB antisen	c 165	11.2	62.2	28	22	AA502175	Partial DNA #7 enc
c 93	11.4	63.3	21	17	AAI33465	MKP gene antisense	c 166	11.2	62.2	28	22	AAE82040	Xyloglucan endoglu
c 94	11.4	63.3	21	22	AAE9586	Human gene single	c 167	11.2	62.2	28	22	AAE84690	Partial nucleotide
c 95	11.4	63.3	21	22	AAE25861	Human MRP antisens	c 168	11.2	62.2	28	22	AAE77865	Partial XGU endogl
c 96	11.4	63.3	22	22	AAE92242	Human ICERB coding	c 169	11.2	62.2	28	22	AAE79726	Aspergillus aculea
c 97	11.4	63.3	24	24	ABL61087	RNA uncoiling enzy	c 170	11.2	62.2	28	22	AAE81158	Aspergillus aculea
c 98	11.4	63.3	25	22	AAAO7400	PCR primer for C5L	c 171	11.2	62.2	28	22	AAE75779	Partial XGU endogl
c 99	11.4	63.3	25	22	AAH38135	SNP specific SNPE	c 172	11.2	62.2	28	22	AAE77556	Partial XGU endogl
c 100	11.4	63.3	26	22	AA504013	Rhesus gene locus:	c 173	11.2	62.2	28	22	AAE59738	A. aculeatus xylogl
c 101	11.4	63.3	28	22	AAAD20452	P. syringae pv. to	c 174	11.2	62.2	29	17	AAI33579	A. aculeatus CBS 1
c 102	11.4	63.3	29	24	ABK96413	PCR primer OGR25 f	c 175	11.2	62.2	29	17	AAE29638	PCR primer MB108 u
c 103	11.4	63.3	36	24	ABA97262	Mutagenic primer 1	c 176	11.2	62.2	29	20	AAV64110	HSV-2 gH gene PCR
c 104	11.4	63.3	36	24	ABA97262	Mutagenic primer 2	c 177	11.2	62.2	30	12	AAO13244	Splint probe c4bp.
c 105	11.4	63.3	38	16	AAI04582	Sense primer for h	c 178	11.2	62.2	30	21	AA231659	PCR primer for hum
c 106	11.4	63.3	39	22	AAE68818	Human IL4Ralpha ge	c 179	11.2	62.2	32	19	AAV22413	Human telomerase r
c 107	11.4	63.3	39	22	AAE68818	Human IL4Ralpha ge	c 180	11.2	62.2	32	24	AAI68048	Epothilone PKS gen
c 108	11.4	63.3	39	22	AAE68836	Human IL4Ralpha ge	c 181	11.2	62.2	34	20	AAZ00715	Human telomerase c
c 109	11.4	63.3	39	22	AAE69847	Human IL4Ralpha ge	c 182	11.2	62.2	34	21	AAAI1912	Human telomerase c
c 110	11.4	63.3	47	18	AAZ68989	Human map-related	c 183	11.2	62.2	35	20	AAAI6949	CD4+ human T-Lymph
c 111	11.4	63.3	49	18	AAI80464	Hepatoma AS-30D Ty	c 184	11.2	62.2	36	21	AAZ91587	Primer #12 for con
c 112	11.2	62.2	17	24	AAAD23904	Human transferrin	c 185	11.2	62.2	36	24	ABA97265	M13X11 construct
c 113	11.2	62.2	18	21	AAZ36581	Probe hybridizing	c 186	11.2	62.2	36	24	ABA97265	Mutagenic primer 1
c 114	11.2	62.2	18	24	ABLA4392	Human chromosome 1	c 187	11.2	62.2	37	14	AAO49129	Mutagenic primer 2
c 115	11.2	62.2	20	15	AAO55806	anol gene primer.	c 188	11.2	62.2	38	22	AAH49077	A. pleuropneumonia
c 116	11.2	62.2	20	20	AAOX09055	Tumour necrosis fa	c 189	11.2	62.2	41	19	AAV37843	Human IDLR gene as
c 117	11.2	62.2	20	22	AAH76243	Human macrophage-d	c 190	11.2	62.2	41	20	AAK56674	CD4+ human T-Lymph
c 118	11.2	62.2	20	22	AAH81191	Human bcl-6 phosph	c 191	11.2	62.2	42	13	AAO21357	Primer 47. Synthe
c 119	11.2	62.2	20	22	ABK51698	Human CCR receptor	c 192	11.2	62.2	42	18	AAV02266	IL-6R CCR primer p
c 120	11.2	62.2	21	21	AAZ88066	Human zcaci-1 PCR	c 193	11.2	62.2	42	18	AAE86099	Human parathyroid
c 121	11.2	62.2	21	21	AAZ60648	PCR primer used to	c 194	11.2	62.2	44	24	AB182083	K-ras mutation det
c 122	11.2	62.2	21	22	AAAC85762	PCR primer used to	c 195	11.2	62.2	45	8	AAI70499	Consensus repeat s
c 123	11.2	62.2	21	22	AAAC85762	Proclactin reverse	c 196	11.2	62.2	45	22	AAE85184	PCR primer for DNA
c 124	11.2	62.2	21	22	AAE97639	Human gene single	c 197	11.2	62.2	46	22	AAE85186	PCR primer for DNA
c 125	11.2	62.2	21	24	ABK65421	Human single nucle	c 198	11.2	62.2	47	21	AAZ68421	Human map-related
c 126	11.2	62.2	22	18	AAI65390	Primer for C-termi	c 199	11.2	62.2	47	21	AAZ68456	Human map-related
c 127	11.2	62.2	22	21	AAAC04474	Human DAXX gene ex	c 200	11.2	62.2	48	15	AAO62437	Vector pVAC1 const
c 128	11.2	62.2	23	21	AAAC67954	Rat Erba receptor	c 201	11.2	62.2	50	22	AAI29784	Human SNP oligonuc
c 129	11.2	62.2	24	15	AAO77751	Beta-actin PCR pri	c 202	11.2	62.2	50	22	AAI30994	Human SNP oligonuc
c 130	11.2	62.2	24	21	AAAC63899	Chinese hamster be	c 203	11.2	62.2	50	22	AAI76591	Human silent SNP c
c 131	11.2	62.2	24	21	AAAC63901	Rat beta-actin RT-	c 204	11.2	61.1	15	24	ABL8317	Human CHRE allele
c 132	11.2	62.2	24	21	AAAG95888	Reverse PCR primer	c 205	11.2	61.1	17	18	AAV75252	Mouse flt-1 VEGF r
c 133	11.2	62.2	24	21	AAAI2788	PCR primer ace28c	c 206	11.2	61.1	18	18	AAK75648	Mouse flt-1 VEGF r
c 134	11.2	62.2	24	22	AAI71185	Human beta actin p	c 207	11.2	61.1	20	22	AAE73035	Human dxxx inhibit
c 135	11.2	62.2	24	22	AA507960	Human G-protein co	c 208	11.2	61.1	27	13	AAO22942	Sequence of primer
c 136	11.2	62.2	24	22	AA508276	Human G-protein co	c 209	11.2	61.1	27	14	AAO48200	PCR primer for amp
c 137	11.2	62.2	24	22	AAE82281	Human beta CDNA PC	c 210	11.2	61.1	27	14	AAH78840	Muski380F primer u
c 138	11.2	62.2	24	22	AAE30649	Human HOGFX hyprid	c 211	11.2	61.1	27	22	AAH78840	PCR primer used to
c 139	11.2	62.2	24	22	AAE30652	Human HOGFX hyprid	c 212	11.2	61.1	27	22	AAE85341	Human A-Raf hamme
c 140	11.2	62.2	24	24	ABN88996	Human beta-actin p	c 213	11.2	61.1	29	20	AAV92263	Human genomic DNA
c 141	11.2	62.2	24	24	ABK50042	Beta actin reverse	c 214	11.2	61.1	38	10	AAAG4509	Probe for N-termin
c 142	11.2	62.2	24	24	ABK50044	Rat beta actin rev	c 215	11.2	61.1	39	22	AAE69788	Human IL4Ralpha po
c 143	11.2	62.2	24	24	ABK70046	Antibody productio	c 216	11.2	61.1	39	22	AAE69795	Human IL4Ralpha po
c 144	11.2	62.2	24	24	ABK70048	NH4-alpha protein	c 217	11.2	61.1	42	15	AAO69251	Human ferredoxin g
c 145	11.2	62.2	24	24	ABK47946	Beta 1,3-N-acetylgl	c 218	11.2	61.1	42	15	AAE63713	Human ferredoxin g
c 146	11.2	62.2	24	24	ABL50788	ace28c PCR primer	c 219	11.2	61.1	42	20	AAAI17001	Test sequence from
c 147	11.2	62.2	24	24	AAAD32610	oligonucleotide ad	c 220	11.2	61.1	42	24	ABK82482	DNA binding molecu
c 148	11.2	62.2	25	24	ABO03457	Human Klu6 PCR pri	c 221	10.8	60.0	15	22	AAE69569	Human IL4Ralpha ge
c 149	11.2	62.2	25	22	AAE31891	Fungal probe SEQ ID	c 222	10.8	60.0	15	22	AAE49082	IGF-1 oligonucleot
c 150	11.2	62.2	25	24	ABN99557	Fungal probe SEQ ID	c 223	10.8	60.0	15	22	AAE49084	IGF-1 oligonucleot
c 151	11.2	62.2	25	24	ABN99575	Penicillium citrin	c 224	10.8	60.0	15	22	AAE52896	IGF-1 oligonucleot
c 152	11.2	62.2	25	24	ABK29154	Penicillium janthi	c 225	10.8	60.0	16	15	AAE52898	Bifidobacterium an
c 153	11.2	62.2	25	24	ABK29172	Human catalytic te	c 226	10.8	60.0	16	15	AAO56019	Bifidobacterium an
c 154	11.2	62.2	26	20	AAV72136	Human catalytic te	c 227	10.8	60.0	16	15	AAO56020	Bifidobacterium bt
c 155	11.2	62.2	26	20	AAV72140	Human catalytic te	c 228	10.8	60.0	16	15	AAO56022	Bifidobacterium in

229	10.8	60.0	16	15	AA056023	Bifidobacterium lo	c 302	10.8	60.0	31	22	AA130846	Human single nucle
230	10.8	60.0	16	24	ABU51557	Human replication	c 303	10.8	60.0	31	22	AA131266	Human single nucle
231	10.8	60.0	16	24	ABK29389	Penicillium olsoni	c 304	10.8	60.0	31	24	ABK52374	Glucose dehydrogen
232	10.8	60.0	17	18	AAx73280	Mouse Flk-1 VEGF r	c 305	10.8	60.0	31	24	ABK52374	Human ERG DNazyme,
233	10.8	60.0	17	18	AAx73279	Mouse Flk-1 VEGF r	c 306	10.8	60.0	32	15	AAQ78763	Primer OMB19. Syn
234	10.8	60.0	17	24	ABN01477	Human GDM-LP-1 17-m	c 307	10.8	60.0	32	15	AAQ78763	Human alpha-galact
235	10.8	60.0	17	24	ABN01481	Human GDM-LP-1 17-m	c 308	10.8	60.0	32	15	AAQ66244	Alpha-galactosidas
236	10.8	60.0	17	24	ABN02219	Human GDM-LP-1 17-m	c 309	10.8	60.0	34	17	AAQ59161	Primer for amplifly
237	10.8	60.0	17	24	ABN02220	Human GDM-LP-1 17-m	c 310	10.8	60.0	34	17	AAQ59161	SRE-2BP DNA bindin
238	10.8	60.0	17	24	ABN02221	Human GDM-LP-1 17-m	c 311	10.8	60.0	36	19	AAV18765	Primer LF394 for c
239	10.8	60.0	17	24	ABN02222	Human GDM-LP-1 17-m	c 312	10.8	60.0	37	22	AAH70278	Human cervical can
240	10.8	60.0	17	24	ABK17953	Human ERG hammethe	c 313	10.8	60.0	40	20	AA219800	D. melanogaster ant
241	10.8	60.0	17	24	ABK18758	Human ERG DNazyme	c 314	10.8	60.0	40	21	AA207766	PCR primer 9BP. 6Q
242	10.8	60.0	17	24	ABU30538	Human H7A genotcyp1	c 315	10.8	60.0	40	20	AA236513	Diabody primer LIN
243	10.8	60.0	18	7	AAAN60539	Sequence of probe	c 316	10.8	60.0	41	15	AAQ68309	Primer 46. Synthe
244	10.8	60.0	18	21	AAZ01332	PCR primer for Pgl	c 317	10.8	60.0	41	15	AAQ56673	Primer RhuVlamdbd
245	10.8	60.0	19	21	AAAZ2682	PCR primer for amp	c 318	10.8	60.0	42	13	AAQ23843	Primer RhuVlamdbd
246	10.8	60.0	19	21	AAZ43827	Human fetal brain	c 319	10.8	60.0	42	13	AAQ23843	Primer RhuVlamdbd
247	10.8	60.0	19	23	AAAS13749	Simple sequence re	c 320	10.8	60.0	42	13	AAQ23848	Human RhuVlamdbd
248	10.8	60.0	20	17	AAAT13325	IGF 1R ATP-directe	c 321	10.8	60.0	42	24	AAQ28857	Human antibody cha
249	10.8	60.0	20	17	AAAT13326	IGF 1R ATP-directe	c 322	10.8	60.0	42	24	AAQ28857	Human antibody cha
250	10.8	60.0	20	19	AAV57182	Human Notch-3 muta	c 323	10.8	60.0	43	24	AAQ28858	p53 mutation detec
251	10.8	60.0	20	19	AAV57101	Human Notch3 mutan	c 324	10.8	60.0	47	20	AA201092	Probe for human PG
252	10.8	60.0	20	19	AAZ11938	Human potassium ch	c 325	10.8	60.0	47	20	AA201092	PCR primer for det
253	10.8	60.0	20	20	AAAZ7171	F probe for human GM	c 326	10.8	60.0	47	21	AAAZ7169	VEGF 2'-NH2-RNA nu
254	10.8	60.0	20	21	AAAZ7184	Probe for human AP-PC	c 327	10.8	60.0	48	15	AAQ62436	Human SNP oligonuc
255	10.8	60.0	20	24	ABN85571	Human beta actin p	c 328	10.8	60.0	50	22	AAI75339	Human silent SNP c
256	10.8	60.0	20	24	ABK69390	Chimeric phosphoro	c 329	10.8	60.0	50	22	AAI75339	Human transcriptio
257	10.8	60.0	20	24	ABAO2226	Human/mouse C/EBP	c 330	10.8	60.0	50	22	AAI75339	Human silent SNP c
258	10.8	60.0	21	17	AAI16424	Primer #1 for SWSS	c 331	10.8	60.0	50	22	AAI75339	Human transcriptio
259	10.8	60.0	21	17	AAZ28423	Plus strand PCR pr	c 332	10.8	60.0	50	22	AAI75339	Human transcriptio
260	10.8	60.0	21	20	AAAZ9022	Human transcriptio	c 333	10.8	60.0	50	22	AAI75339	Human transcriptio
261	10.8	60.0	21	21	AAAC62619	Human OB gene sequ	c 334	10.8	60.0	50	22	AAI75339	Human transcriptio
262	10.8	60.0	21	21	AAAC62619	Human OB gene sequ	c 335	10.8	60.0	50	22	AAI75339	Human transcriptio
263	10.8	60.0	21	21	AAAI2341	Human OB DNA PCR p	c 336	10.8	60.0	50	22	AAI75339	Human transcriptio
264	10.8	60.0	22	17	AAAT33366	Poly(ADP-ribose) P	c 337	10.8	60.0	50	22	AAI75339	Human transcriptio
265	10.8	60.0	22	22	AAV65148	Ehrlichia sp. E80	c 338	10.8	60.0	50	22	AAI75339	Human transcriptio
266	10.8	60.0	22	22	AAE76131	Human CPTFR real-tl	c 339	10.8	60.0	50	22	AAI75339	Human transcriptio
267	10.8	60.0	22	23	AAZ02190	Tail primer #14 fir	c 340	10.8	60.0	50	22	AAI75339	Human transcriptio
268	10.8	60.0	23	23	ABK22664	Pregnancy associat	c 341	10.8	60.0	50	22	AAI75339	Human transcriptio
269	10.8	60.0	23	24	ABK22664	Human ERG Genebioc	c 342	10.8	60.0	50	22	AAI75339	Human transcriptio
270	10.8	60.0	23	24	ABK22664	Human ERG Genebioc	c 343	10.8	60.0	50	22	AAI75339	Human transcriptio
271	10.8	60.0	24	22	AAE55566	PCR primer used to	c 344	10.8	60.0	50	22	AAI75339	Human transcriptio
272	10.8	60.0	24	22	ABN04406	Human GDM-LP-1 25-m	c 345	10.8	60.0	50	22	AAI75339	Human transcriptio
273	10.8	60.0	25	24	ABN04418	Human GDM-LP-1 25-m	c 346	10.8	60.0	50	22	AAI75339	Human transcriptio
274	10.8	60.0	25	24	ABN05148	Human GDM-LP-1 25-m	c 347	10.8	60.0	50	22	AAI75339	Human transcriptio
275	10.8	60.0	25	24	ABN05149	Human GDM-LP-1 25-m	c 348	10.8	60.0	50	22	AAI75339	Human transcriptio
276	10.8	60.0	25	24	ABN05150	Human GDM-LP-1 25-m	c 349	10.8	60.0	50	22	AAI75339	Human transcriptio
277	10.8	60.0	25	24	ABN05151	Human GDM-LP-1 25-m	c 350	10.8	60.0	50	22	AAI75339	Human transcriptio
278	10.8	60.0	25	24	ABN05152	Human GDM-LP-1 25-m	c 351	10.8	60.0	50	22	AAI75339	Human transcriptio
279	10.8	60.0	25	24	ABN05153	Human GDM-LP-1 25-m	c 352	10.8	60.0	50	22	AAI75339	Human transcriptio
280	10.8	60.0	25	24	ABN05154	Human GDM-LP-1 25-m	c 353	10.8	60.0	50	22	AAI75339	Human transcriptio
281	10.8	60.0	25	24	ABN05155	Human GDM-LP-1 25-m	c 354	10.8	60.0	50	22	AAI75339	Human transcriptio
282	10.8	60.0	25	24	ABN05156	Human GDM-LP-1 25-m	c 355	10.8	60.0	50	22	AAI75339	Human transcriptio
283	10.8	60.0	25	24	ABN05157	Human GDM-LP-1 25-m	c 356	10.8	60.0	50	22	AAI75339	Human transcriptio
284	10.8	60.0	25	24	ABN05158	Human GDM-LP-1 25-m	c 357	10.8	60.0	50	22	AAI75339	Human transcriptio
285	10.8	60.0	26	18	AAE28790	Human GDM-LP-1 25-m	c 358	10.8	60.0	50	22	AAI75339	Human transcriptio
286	10.8	60.0	26	18	AAE28790	Human GDM-LP-1 25-m	c 359	10.8	60.0	50	22	AAI75339	Human transcriptio
287	10.8	60.0	26	22	AAE28791	Hafrpin nucleic ac	c 360	10.8	60.0	50	22	AAI75339	Human transcriptio
288	10.8	60.0	26	22	AAE28791	Human GABA(b) rece	c 361	10.8	60.0	50	22	AAI75339	Human transcriptio
289	10.8	60.0	26	22	AAE17071	Information carryl	c 362	10.8	60.0	50	22	AAI75339	Human transcriptio
290	10.8	60.0	26	22	AAE17071	G protein-coupled	c 363	10.8	60.0	50	22	AAI75339	Human transcriptio
291	10.8	60.0	28	24	ABK66752	Human gene specifl	c 364	10.8	60.0	50	22	AAI75339	Human transcriptio
292	10.8	60.0	29	20	AAK83535	Primer A3 P2491/Q2	c 365	10.8	60.0	50	22	AAI75339	Human transcriptio
293	10.8	60.0	29	20	AAK83535	Primer A3 P2491/Q2	c 366	10.8	60.0	50	22	AAI75339	Human transcriptio
294	10.8	60.0	29	21	AAAG9101	Primer Lowa3 for m	c 367	10.8	60.0	50	22	AAI75339	Human transcriptio
295	10.8	60.0	29	21	AAAG9103	Human Rab24 PCR pr	c 368	10.8	60.0	50	22	AAI75339	Human transcriptio
296	10.8	60.0	29	21	AAAG9103	Human Rab24 PCR pr	c 369	10.8	60.0	50	22	AAI75339	Human transcriptio
297	10.8	60.0	29	24	ABN81596	Escherichia coli w	c 370	10.8	60.0	50	22	AAI75339	Human transcriptio
298	10.8	60.0	30	20	AAZ30466	Human FGF23 protei	c 371	10.8	60.0	50	22	AAI75339	Human transcriptio
299	10.8	60.0	30	20	AAZ30466	Primer 19 for toba	c 372	10.8	60.0	50	22	AAI75339	Human transcriptio
300	10.8	60.0	30	20	AAZ30466	Human Silt-1 PCR p	c 373	10.8	60.0	50	22	AAI75339	Human transcriptio
301	10.8	60.0	31	22	AAI29594	Human hdbD-1 contr	c 374	10.8	60.0	50	22	AAI75339	Human transcriptio
						Human single nucle							

C 375	10.6	58.9	21	17	AAT10459	Anti-HIV TAR regio	C 448	10.6	58.9	38	21	AAZ55102	Neisseria species
C 376	10.6	58.9	21	18	AAT92446	TAT system oligonu	449	10.6	58.9	38	22	AAF31703	Human NF-AT polyu
C 377	10.6	58.9	21	18	AAT64326	Antisense oligonuc	450	10.6	58.9	38	24	AAD34029	Human probe #19 fo
C 378	10.6	58.9	21	19	AAV48412	Transforming growt	C 451	10.6	58.9	39	22	AAF69796	Human IL4Rbeta po
C 379	10.6	58.9	21	19	AAV38643	Human ICAM-1, E-se	C 452	10.6	58.9	40	12	AAQ11990	Probe Sg918 to ena
C 380	10.6	58.9	21	22	AAI66658	Human CERP DNA rel	C 453	10.6	58.9	40	18	AAT87125	IFN-gamma 2' F RNA
C 381	10.6	58.9	21	22	AAF95645	Human gene single	C 454	10.6	58.9	40	20	AAAZ24048	Human b7x PCR prim
C 382	10.6	58.9	21	22	AAF97241	Human gene single	C 455	10.6	58.9	41	14	AAQ52409	Nucleic acid ligan
C 383	10.6	58.9	21	24	ABK70958	Mouse HYPLIP1 locu	C 456	10.6	58.9	41	17	AAT07720	Human TNF PCR prim
C 384	10.6	58.9	21	24	ABK68054	Mouse HYPLIP1 locu	C 457	10.6	58.9	41	17	AAV00805	SELEX ligand 1.3c
C 385	10.6	58.9	23	14	AAQ45574	Sequence of PCR pr	C 458	10.6	58.9	41	19	AAV14590	Random region 1.3c
C 386	10.6	58.9	23	20	AAZ39452	Plasmid pSCFV31 co	C 459	10.6	58.9	41	20	AAV79665	RNA ligand sequenc
C 387	10.6	58.9	23	20	AAZ23989	Plasmid pSCFV 31 p	C 460	10.6	58.9	41	21	AAAZ2765	High-affinity nucl
C 388	10.6	58.9	23	22	AAH75613	Human crn-Like gen	C 461	10.6	58.9	41	24	ABA39918	Human TNF PCR prim
C 389	10.6	58.9	24	16	AAH05419	Human TGF-beta1 mr	C 462	10.6	58.9	41	24	ABK61141	SELEX process nucl
C 390	10.6	58.9	24	16	AAQ75041	Human TGF-beta(1)	C 463	10.6	58.9	41	24	AAZ52011	Human hsp dependen
C 391	10.6	58.9	24	17	AAT18698	CDNA3 antisense pr	C 464	10.6	58.9	42	13	AAQ35677	IL3 promoter eleme
C 392	10.6	58.9	24	20	AAK35817	PCR primer for mou	C 465	10.6	58.9	42	14	AAQ50255	HIV env INS mutage
C 393	10.6	58.9	24	21	AAZ35967	Cytochrome P450 cy	C 466	10.6	58.9	42	18	AAT47159	Primer JCA158 used
C 394	10.6	58.9	24	24	AAK99320	Ferritin 14 protei	C 467	10.6	58.9	42	18	AAT47164	Primer JCA158 used
C 395	10.6	58.9	24	24	ABO03479	Oligonucleotide ad	C 468	10.6	58.9	42	20	AAK31929	Human nodal DNA am
C 396	10.6	58.9	24	24	ABI82402	Capture oligonucle	C 469	10.6	58.9	42	21	AAZ47012	Primer JCA158 for
C 397	10.6	58.9	24	24	ABI82403	Capture oligonucle	C 470	10.6	58.9	42	24	ABA97892	GFP-seguroin linke
C 398	10.6	58.9	24	24	ABI91668	Capture oligonucle	C 471	10.6	58.9	43	19	AAV36842	Self-cleaving G8 D
C 399	10.6	58.9	24	24	ABI91669	Capture oligonucle	C 472	10.6	58.9	43	20	AAV84742	Antibody heavy cha
C 400	10.6	58.9	24	24	ABI92598	Capture oligonucle	C 473	10.6	58.9	44	22	AAH77159	Rat VL30 packaging
C 401	10.6	58.9	24	24	ABI92599	Capture oligonucle	C 474	10.6	58.9	44	22	AAH23283	3x2F ZGS zinc fing
C 402	10.6	58.9	24	24	ABI92788	Capture oligonucle	C 475	10.6	58.9	45	16	AAH01086	VJuns-rev11B cons
C 403	10.6	58.9	24	24	ABI92789	Capture oligonucle	C 476	10.6	58.9	45	16	AAO83912	Hepatitis C virus
C 404	10.6	58.9	26	19	AAV37879	PCR primer used to	C 477	10.6	58.9	45	17	AAT16672	Hepatitis C virus
C 405	10.6	58.9	26	19	AAV35016	Primer for human C	C 478	10.6	58.9	46	22	AAH01946	parc resistance ge
C 406	10.6	58.9	26	19	AAV20685	TAR mmetic oligon	C 479	10.6	58.9	46	24	ABK52805	Human prodynorphin
C 407	10.6	58.9	26	21	AAAO8096	Riesus CD11a I-dom	C 480	10.6	58.9	47	19	AAV56425	Human ICAM-R CDNA
C 408	10.6	58.9	26	21	AAZ54653	Neisseria species	C 481	10.6	58.9	47	21	AAA97167	CDR2 nucleotide se
C 409	10.6	58.9	26	24	ABK66928	Human gene specifi	C 482	10.6	58.9	47	21	AAAO8313	Murine ICR-1.1 ant
C 410	10.6	58.9	27	16	AAT02373	Primer DVI derived	C 483	10.6	58.9	47	21	AAZ48313	Humanised murine a
C 411	10.6	58.9	27	20	AAH81374	HIV-1 BRU tal gene	C 484	10.6	58.9	47	23	AAH24339	CNS disorder-relat
C 412	10.6	58.9	28	13	AAQ31588	PCR primer for the	C 485	10.6	58.9	49	22	AAH86365	Human schizophre
C 413	10.6	58.9	28	20	AAZ32514	PCR primer RelB-P3	C 486	10.6	58.9	50	22	AAAC91231	Human SNP oligonuc
C 414	10.6	58.9	28	21	AAZ49427	5' primer BCK1 for	C 487	10.6	58.9	50	22	AAL31527	Human SNP oligonuc
C 415	10.6	58.9	28	22	AAH57337	Polymorphic fragme	C 488	10.6	58.9	50	22	AAL34259	Human SNP oligonuc
C 416	10.6	58.9	29	11	AAAO4117	TRKRG9PST primer f	C 489	10.6	58.9	50	22	AAI75587	Human silent SNP c
C 417	10.6	58.9	30	11	AAQ04634	PCR primer for tru	C 490	10.6	58.9	50	23	AAH23287	3x2F ZGL zinc fing
C 418	10.6	58.9	30	14	AAQ41177	EBP primer 386-4.	C 491	10.6	58.9	50	23	ABL00153	Human silent nonco
C 419	10.6	58.9	30	15	AAQ63761	Beta-cardiac myosi	C 492	10.4	57.8	14	10	AAAN94504	Probe for N-termin
C 420	10.6	58.9	30	16	AAO91122	Interleukin-12 p-3	C 493	10.4	57.8	15	16	AAT55760	Human TNF-alpha ha
C 421	10.6	58.9	30	17	AAT14254	eck receptor bindi	C 494	10.4	57.8	15	16	AAT52162	Human ICAM hammerh
C 422	10.6	58.9	30	18	AAT43766	T-cell receptor-ga	C 495	10.4	57.8	15	21	AAZ63420	C-1027 gene cluste
C 423	10.6	58.9	30	20	AAZ25301	Mouse spingostine	C 496	10.4	57.8	15	21	AAZ64230	Substrate for hamm
C 424	10.6	58.9	30	21	AAZ47169	Human diallelic po	C 497	10.4	57.8	15	22	AAH52899	IGF-I oligonucleot
C 425	10.6	58.9	31	20	AAZ06240	Human single nucle	C 498	10.4	57.8	15	22	AAH52900	IGF-I oligonucleot
C 426	10.6	58.9	31	22	AAI30081	Human single nucle	C 499	10.4	57.8	15	24	ABK09879	P2RY1 gene allele-
C 427	10.6	58.9	31	22	AAI30221	Human single nucle	C 500	10.4	57.8	18	16	AAT56721	Human TNF-alpha ha
C 428	10.6	58.9	32	10	ABN85334	Human Bone Marrow	C 501	10.4	57.8	18	18	AAT76293	Human cathepsin G
C 429	10.6	58.9	33	17	AAT42149	HIV-1 gp120 V3 loo	C 502	10.4	57.8	18	19	AAV32491	Bovine retinaldehy
C 430	10.6	58.9	33	19	AAV00534	HIV-1 gp120 DNA pr	C 503	10.4	57.8	18	20	AAZ18056	HB gene GBX 2 spec
C 431	10.6	58.9	33	20	AAAZ56200	Human alpha-7 nico	C 504	10.4	57.8	18	20	AAAZ4087	Human cathepsin G
C 432	10.6	58.9	33	21	AAAI5885	Rhesus monkey mela	C 505	10.4	57.8	18	20	AAAF19653	Human cathepsin G
C 433	10.6	58.9	33	24	AAZ45323	PCR primer for GDP	C 506	10.4	57.8	18	21	AAAZ3531	Low adenosine anti
C 434	10.6	58.9	33	24	ABL57838	Human beta-actin p	C 507	10.4	57.8	18	21	AAZ58853	Bovine retinaldehy
C 435	10.6	58.9	33	24	ABK12120	Human hRRTI PCR pr	C 508	10.4	57.8	19	19	AAV57786	Human chromosome 1
C 436	10.6	58.9	34	14	AAQ52074	Breast cancer spec	C 509	10.4	57.8	20	16	AAQ82617	Chromosome 11 (loc
C 437	10.6	58.9	34	22	AAH41280	Acetyltransferase	C 510	10.4	57.8	20	17	AAT32608	BKCA1 gene mapping
C 438	10.6	58.9	34	22	AAAF23029	M. tuberculosis 23	C 511	10.4	57.8	20	17	AAT17537	Primer #1 for tand
C 439	10.6	58.9	34	22	AAAF23031	Human silent SNP c	C 512	10.4	57.8	20	17	AAT18321	BKCA1 gene mapping
C 440	10.6	58.9	35	22	AAI78919	Human simplex vir	C 513	10.4	57.8	20	19	AAV18603	Synthetic human tu
C 441	10.6	58.9	37	17	AAAT47995	Herpes simplex vir	C 514	10.4	57.8	20	20	AAAZ2050	PCR primer used to
C 442	10.6	58.9	37	20	AAZ29931	Herpes simplex vir	C 515	10.4	57.8	20	20	AAAZ3591	Oligonucleotide ta
C 443	10.6	58.9	37	20	AAV72561	Sequence of probe	C 516	10.4	57.8	20	21	AAAZ29856	Human jun N-termin
C 444	10.6	58.9	38	14	AAO40320	NF-AT transcriptio	C 517	10.4	57.8	20	21	AAAZ0987	Human TNFalpha ant
C 445	10.6	58.9	38	16	AAO86685	Human nuclear fact	C 518	10.4	57.8	20	21	AAA41139	Human TNFalpha ant
C 446	10.6	58.9	38	21	AAZ29271	T. brucei trypanos	C 519	10.4	57.8	20	22	AAD10590	Human WMP2 chimeri
C 447	10.6	58.9	38	21	AAA12115		C 520	10.4	57.8	20	22	AAZ07536	REVOLUTA cDNA PCR

C 521	10.4	57.8	20	22	AAH39565	SNP specific upper	594	10.4	57.8	38	14	AAO39347	VH-CH1 repeatolice
C 522	10.4	57.8	20	22	AAF98473	Human IGFBP gene p	595	10.4	57.8	38	16	AAH53833	Rat ICM hammerhead
523	10.4	57.8	20	24	ABK94887	Fat regulated gene	C 596	10.4	57.8	38	21	AAH50727	Primer TOP2-431r f
524	10.4	57.8	20	24	ABH94349	Mouse C/EBP beta p	C 597	10.4	57.8	38	24	AAK98445	Human V gene 11bra
525	10.4	57.8	20	24	ABK29413	Penicillium sclero	C 598	10.4	57.8	40	18	AAH97407	Synthetic oligomer
C 527	10.4	57.8	21	21	AAH88423	Primer #1 used to	C 599	10.4	57.8	41	24	ABH89505	Human snRNP access
C 528	10.4	57.8	21	22	AAH26264	Human COL9A1 PCR p	C 600	10.4	57.8	45	17	AAH34003	Primer for beta ch
C 529	10.4	57.8	21	22	AAH62640	Interferon recepto	C 601	10.4	57.8	47	20	AAH56555	Primer 28. Synthe
530	10.4	57.8	21	22	AAH21633	Human RRS homology	C 602	10.4	57.8	50	18	AAH61580	VH and scrv antibo
531	10.4	57.8	21	22	AAH95766	Human gene single	C 603	10.4	57.8	50	18	AAH61580	scrv antibody 11br
C 532	10.4	57.8	21	22	AAH95820	Human gene single	C 604	10.4	57.8	50	22	AAH29466	Human SNP oligonc
C 533	10.4	57.8	22	15	AAO65757	Type II procollase	C 605	10.4	57.8	50	22	AAH32035	Human SNP oligonc
534	10.4	57.8	22	24	ABO62255	Mouse synectin 4 i	C 606	10.2	56.7	16	18	AAH92447	TAT system oligonu
535	10.4	57.8	22	24	ABH95593	Human G-protein co	C 607	10.2	56.7	17	18	AAH92447	Mouse flt-1-VEGF r
536	10.4	57.8	23	13	AAO23701	Primer HUH2ABACK	C 608	10.2	56.7	17	18	AAH92447	TAT system oligonu
537	10.4	57.8	23	13	AAO32276	Human heavy chain	C 609	10.2	56.7	17	21	AAH92451	Hammerhead ribozym
538	10.4	57.8	23	14	AAO39334	VH domain PCR amp1	C 610	10.2	56.7	17	21	AAH92451	Hammerhead ribozym
539	10.4	57.8	23	14	AAO48988	Multimeric (SBP) a	C 611	10.2	56.7	17	24	ABH09236	Human GDMLP-1 17-m
540	10.4	57.8	23	16	AAH29178	HuVh2a 5' heavy ch	C 612	10.2	56.7	17	24	ABH09237	Human GDMLP-1 17-m
541	10.4	57.8	23	21	AAZ43844	Human IgG4 heavy c	C 613	10.2	56.7	17	24	ABH09238	Human GDMLP-1 17-m
542	10.4	57.8	23	22	ABH03073	PCR primer Hu VH2-	C 614	10.2	56.7	18	18	AAH75547	Mouse flt-1-VEGF r
543	10.4	57.8	23	22	AAH20056	Human antibody VH	C 615	10.2	56.7	18	20	AAH23111	Primer #34. Synth
544	10.4	57.8	23	22	AAH13301	Human VH domain am	C 616	10.2	56.7	18	21	AAH286823	Human Smad1 antise
C 545	10.4	57.8	23	22	AAH13301	Human VH domain am	C 617	10.2	56.7	18	24	ABH88163	Rabbit beta-globin
546	10.4	57.8	23	22	AAH06824	Human VH domain am	C 618	10.2	56.7	19	20	AAH90634	Primer FIV5 to Int
547	10.4	57.8	23	23	ABH87304	Protein kinase CDN	C 619	10.2	56.7	19	20	AAH37253	Human D1ST gene sp
548	10.4	57.8	23	24	ABK93296	Human androgen rec	C 620	10.2	56.7	19	21	AAH38233	HIV-1 tat gene rib
549	10.4	57.8	23	24	ABK51872	PCR primer #2 for	C 621	10.2	56.7	19	22	AAH15493	Human NOVX7 DNA in
550	10.4	57.8	23	24	AAK98427	Human V gene 11bra	C 622	10.2	56.7	19	22	AAH15494	Human NOVX7 DNA in
551	10.4	57.8	23	24	AAK98427	Human V gene 11bra	C 623	10.2	56.7	19	22	AAH24034	HIV tat exon 1 o11
552	10.4	57.8	23	24	AAH30848	PCR primer HUH2B	C 624	10.2	56.7	19	22	AAH24107	Flexibacter maritl
553	10.4	57.8	23	24	AAH28817	Human antibody VH	C 625	10.2	56.7	19	23	ABH10767	Human prostate exp
554	10.4	57.8	24	20	AAH24689	Llama IgG2-specific	C 626	10.2	56.7	19	24	ABH60641	Packaging expressi
C 555	10.4	57.8	24	20	AAH23451	Human TRK3 KACE p	C 627	10.2	56.7	20	13	AAH026641	Primer PEL. Synth
C 556	10.4	57.8	24	21	AAH37154	Human TRK3 KACE p	C 628	10.2	56.7	20	14	AAH035281	PMV primer 5' S
C 557	10.4	57.8	24	21	AAH24573	Non-human animal b	C 629	10.2	56.7	20	15	AAH044577	Antisense oligonc
C 558	10.4	57.8	24	21	AAH24573	Primer #8 used in	C 630	10.2	56.7	20	16	AAH01806	Peptide nucleic ac
559	10.4	57.8	24	24	ABK67119	Human gene specific	C 631	10.2	56.7	20	17	AAH33082	Antisense oligonc
560	10.4	57.8	24	24	ABK01698	Oligonucleotide ad	C 632	10.2	56.7	20	18	AAH65494	CAV immunogenic pe
561	10.4	57.8	24	24	ABH07305	Oligonucleotide ad	C 633	10.2	56.7	20	19	AAH16991	Human telomerase r
C 562	10.4	57.8	24	24	ABH07346	Oligonucleotide ad	C 634	10.2	56.7	20	20	AAH30509	PCR primer used to
C 563	10.4	57.8	25	13	AAH34326	Downstream PCR pr1	C 635	10.2	56.7	20	20	AAH202391	PCR primer used to
C 564	10.4	57.8	25	22	AAH20181	Yeast CPA2 mutant	C 636	10.2	56.7	20	20	AAH94146	PCR primer used to
C 565	10.4	57.8	25	22	AAH20182	Yeast CPA2 mutant	C 637	10.2	56.7	20	20	AAH33586	Oligonucleotide ta
C 566	10.4	57.8	25	22	AAH20182	Yeast CPA2 mutant	C 638	10.2	56.7	20	20	AAH33589	PCR primer for CDK
C 567	10.4	57.8	25	22	AAH14314	Overlapping oligon	C 639	10.2	56.7	20	20	AAH30220	Human CDKN1A genot
C 568	10.4	57.8	25	24	AAH37758	Real-time Validati	C 640	10.2	56.7	20	20	AAH18958	Non-B, non-C, non-
C 569	10.4	57.8	26	14	AAH38382	Sequence of oligo	C 641	10.2	56.7	20	21	AAH93244	Mouse STAT3 phosph
C 570	10.4	57.8	27	12	AAH10665	HLA Class II locus	C 642	10.2	56.7	20	21	AAH93294	Human STAT3 phosph
571	10.4	57.8	27	22	AAH12718	Human AHC 2H01 CDN	C 643	10.2	56.7	20	21	AAH57510	Dog genomic marker
572	10.4	57.8	28	22	AAH12654	Human AHC 2H01 CDN	C 644	10.2	56.7	20	21	AAH66267	TRAF6 antisense ol
573	10.4	57.8	28	22	AAH8739	Human catenin-bind	C 645	10.2	56.7	20	21	AAH48849	Human WCAM-1 antls
574	10.4	57.8	29	20	AAH92280	Human C-Raf hamme	C 646	10.2	56.7	20	21	AAH65118	Primer amplifying
575	10.4	57.8	29	20	AAH91474	Human C-Raf hamme	C 647	10.2	56.7	20	21	AAH48640	Reverse primer spe
C 576	10.4	57.8	29	21	AAH93115	Primer used in con	C 648	10.2	56.7	20	21	AAH10987	Human TERT marker
577	10.4	57.8	30	20	AAH23332	N. meningitidis lb	C 649	10.2	56.7	20	22	AAH12349	Human telomerase r
578	10.4	57.8	30	20	AAH23332	N. meningitidis lb	C 650	10.2	56.7	20	22	AAH28496	Human telomerase r
C 579	10.4	57.8	30	20	AAH72200	Human NRC PCR prim	C 651	10.2	56.7	20	22	AAH44276	Human PRO190 rever
580	10.4	57.8	31	19	AAH72201	Human NRC PCR prim	C 652	10.2	56.7	20	22	AAH44276	Human PRO190 rever
C 581	10.4	57.8	31	19	AAH72201	Human NRC PCR prim	C 653	10.2	56.7	20	24	AAH37205	Human MEKK4 antise
582	10.4	57.8	31	21	AAH78639	Primer AADOPRO(+H	C 654	10.2	56.7	20	24	AAH38599	hTERT sense PCR pr
C 583	10.4	57.8	32	12	AAH15522	Human genomic DNA	C 655	10.2	56.7	20	24	AAH35067	Human STAT3 antise
C 584	10.4	57.8	32	12	AAH62324	Primer for amplifi	C 656	10.2	56.7	20	24	AAH35067	Human STAT3 antise
585	10.4	57.8	33	24	ABH84119	Human novel z1nc f	C 657	10.2	56.7	20	24	AAH72484	Human B2F transcri
586	10.4	57.8	35	22	AAH12648	Human TRFR/NGFR 14	C 658	10.2	56.7	20	24	AAH90861	hTERT mRNA primer,
587	10.4	57.8	35	22	AAH12648	Human TRFR/NGFR 14	C 659	10.2	56.7	20	24	AAH90861	Mouse STAT3 antise
588	10.4	57.8	36	16	AAH88733	Human catenin-bind	C 660	10.2	56.7	20	24	AAH96911	Human STAT3 antise
589	10.4	57.8	36	17	AAH50472	Mouse ICAM hammer	C 661	10.2	56.7	20	24	AAH94933	Capture oligonucle
590	10.4	57.8	36	17	AAH50472	Rabbit CERP HH rib	C 662	10.2	56.7	20	24	AAH96314	Capture oligonucle
591	10.4	57.8	36	20	AAH79594	Human CERP HH rib	C 663	10.2	56.7	21	12	AAH12348	3' primer p6 for d
C 592	10.4	57.8	37	22	AAH93084	Amphotropic hyper	C 664	10.2	56.7	21	16	AAH083812	Bacteriophage T7 R
C 593	10.4	57.8	38	13	AAH32286	ABCI polymorphism	C 665	10.2	56.7	21	18	AAH02129	Human steroid 5-a1
						HUHV2BAPPA, a VH b	C 666	10.2	56.7	21	20	AAH08542	Osteocalcin revers

c 667	10.2	56.7	21	21	AAA87929	Human beta-3-adren
c 668	10.2	56.7	21	21	AAZ92065	PCR primer for SST
c 669	10.2	56.7	21	22	AAI64354	PCR primer R2, un
c 670	10.2	56.7	21	24	ABA98246	Primer 12 for sequ
c 671	10.2	56.7	21	24	AA562185	Porcine reverse PC
c 672	10.2	56.7	22	19	AAV06479	Human genomic DNA
c 673	10.2	56.7	23	18	AAV92594	BKRA2 cancer susce
c 674	10.2	56.7	23	22	AAV75433	Codon-optimised HP
c 675	10.2	56.7	23	22	AAV75434	Codon-optimised HP
c 676	10.2	56.7	23	22	AAV46193	Human liver cancer
c 677	10.2	56.7	24	10	AAV90436	Oligonucleotide pr
c 678	10.2	56.7	24	17	AAV38866	Primer for dhat op
c 679	10.2	56.7	24	22	AAV168134	Leptomys centrarchi
c 680	10.2	56.7	24	22	AAV78894	Human ylip28 recep
c 681	10.2	56.7	24	22	AAV08031	Rat SNORF62 recep
c 682	10.2	56.7	24	22	AAV01864	Cytochrome P-450 (
c 683	10.2	56.7	24	24	ABK48513	Human 8.8 protein
c 684	10.2	56.7	24	24	AAV17263	Forward PCR primer
c 685	10.2	56.7	24	24	AB182824	Capture oligonucle
c 686	10.2	56.7	24	24	AB182825	Capture oligonucle
c 687	10.2	56.7	24	24	AB185156	Capture oligonucle
c 688	10.2	56.7	24	24	AB185157	Capture oligonucle
c 689	10.2	56.7	24	24	AB189198	Capture oligonucle
c 690	10.2	56.7	24	24	AB189199	Capture oligonucle
c 691	10.2	56.7	24	24	AB192090	Capture oligonucle
c 692	10.2	56.7	24	24	AB192091	Capture oligonucle
c 693	10.2	56.7	25	14	AAQ52333	Variant peroxidase
c 694	10.2	56.7	25	21	AAA07031	Human integrin bet
c 695	10.2	56.7	25	24	ABN14128	Human GDMLP-1 25-m
c 696	10.2	56.7	25	24	ABN14129	Human GDMLP-1 25-m
c 697	10.2	56.7	25	24	ABN14130	Human GDMLP-1 25-m
c 698	10.2	56.7	25	24	ABN14131	Human GDMLP-1 25-m
c 699	10.2	56.7	25	24	ABN14132	Human GDMLP-1 25-m
c 700	10.2	56.7	25	24	ABN14133	Human GDMLP-1 25-m
c 701	10.2	56.7	25	24	ABN14134	Human GDMLP-1 25-m
c 702	10.2	56.7	25	24	ABN14135	Human GDMLP-1 25-m
c 703	10.2	56.7	25	24	ABN14136	Human GDMLP-1 25-m
c 704	10.2	56.7	25	24	ABN14137	Human GDMLP-1 25-m
c 705	10.2	56.7	25	24	ABN14138	Human GDMLP-1 25-m
c 706	10.2	56.7	26	24	AAK33454	Human TNF-receptor
c 707	10.2	56.7	27	14	AAQ43749	Sequence of primer
c 708	10.2	56.7	27	21	AAV87921	Human beta-3-adren
c 709	10.2	56.7	27	21	AAZ60899	Primer for geranyl
c 710	10.2	56.7	27	22	AAH75615	Human crn-like gen
c 711	10.2	56.7	27	24	ABK15323	PCR primer #2, use
c 712	10.2	56.7	27	24	AAK15764	Adenoviral vector
c 713	10.2	56.7	27	24	ABA89599	Serial analysis of
c 714	10.2	56.7	27	24	ABA89599	Serial analysis of
c 715	10.2	56.7	28	14	AAQ51977	B-cell mRNA ribozy
c 716	10.2	56.7	28	17	AAV28554	Universal bacteria
c 717	10.2	56.7	28	17	AAV38839	Primer for dha3 o
c 718	10.2	56.7	28	19	AAV42034	1,3-Propanediol de
c 719	10.2	56.7	28	19	AAV35755	Synthetic dhaB/dha
c 720	10.2	56.7	28	22	AAZ12527	PCR primer used to
c 721	10.2	56.7	28	22	ABA76949	Universal hybridis
c 722	10.2	56.7	28	22	AAH49543	Human GTP-binding
c 723	10.2	56.7	28	24	ABQ92616	Human leukaemia ch
c 724	10.2	56.7	28	24	ABA89598	Serial analysis of
c 725	10.2	56.7	28	24	ABA89609	Serial analysis of
c 726	10.2	56.7	29	17	AAV42228	Human TBP associat
c 727	10.2	56.7	29	17	AAV33039	Antibody L chain V
c 728	10.2	56.7	29	17	AAV33040	Antibody L chain V
c 729	10.2	56.7	29	17	AAV06785	Human alpha-tropom
c 730	10.2	56.7	29	18	AAV86994	Rt-PCR primer 2 fo
c 731	10.2	56.7	29	18	AAV79610	TATA-binding prote
c 732	10.2	56.7	29	20	AAV77421	PCR primer VLAa5.
c 733	10.2	56.7	29	20	AAV77422	PCR primer VLAa5.
c 734	10.2	56.7	29	21	AAV36971	PCR primer VLAa5.
c 735	10.2	56.7	29	21	AAV36972	PCR primer VLAa5.
c 736	10.2	56.7	29	22	AAH42200	PCR primer for CDN
c 737	10.2	56.7	29	22	AAH42208	PCR primer for CDN
c 738	10.2	56.7	30	22	AAI69875	Erwinia herbicola
c 739	10.2	56.7	30	22	AAI68127	Leptomys centrarchi
c 740	10.2	56.7	30	24	ABA89600	Serial analysis of
c 741	10.2	56.7	30	24	ABA89601	Serial analysis of
c 742	10.2	56.7	30	24	ABA89615	Serial analysis of
c 743	10.2	56.7	30	24	ABA89619	Serial analysis of
c 744	10.2	56.7	31	20	AAV80152	Human beta-1,4-gal
c 745	10.2	56.7	31	20	AAV06239	Human biallelic po
c 746	10.2	56.7	31	20	AAV06223	Human biallelic po
c 747	10.2	56.7	31	21	AAV90586	Herpesvirus salmtr
c 748	10.2	56.7	31	21	AAV79050	Human genomic DNA
c 749	10.2	56.7	31	22	AAV29742	Human single nucle
c 750	10.2	56.7	31	22	AAI29743	Human single nucle
c 751	10.2	56.7	31	22	AAI29923	Human single nucle
c 752	10.2	56.7	31	22	ABK59990	Human single nucle
c 753	10.2	56.7	32	20	AAV31905	Human C1CA1 gene e
c 754	10.2	56.7	32	20	AAV31908	LckBp1 mutants gen
c 755	10.2	56.7	32	22	AAH42185	Nucleotide sequenc
c 756	10.2	56.7	32	24	ABL40396	Primer 4 relative
c 757	10.2	56.7	32	24	ABL40221	Human G protein-co
c 758	10.2	56.7	32	24	ABK13491	DT390 mutagenic ol
c 759	10.2	56.7	33	14	AAQ44329	HTLV-1 amplifier p
c 760	10.2	56.7	33	24	AAV72678	Homo zinc finger p
c 761	10.2	56.7	33	24	ABL50149	Human base mismatch
c 762	10.2	56.7	33	24	AAV17000	Human zinc finger
c 763	10.2	56.7	33	24	ABA96618	Human alpha interf
c 764	10.2	56.7	34	14	AAQ45763	Human prostate tra
c 765	10.2	56.7	34	17	AAV14836	Human prostatic tr
c 766	10.2	56.7	34	20	AAZ10274	Primer ZC4129 used
c 767	10.2	56.7	34	21	AAV99243	PCR primer used to
c 768	10.2	56.7	34	21	AAV53757	Primer used to amp
c 769	10.2	56.7	34	21	AAV72515	PCR primer SQD ID
c 770	10.2	56.7	36	12	AAQ14951	Human aldose reduc
c 771	10.2	56.7	36	17	AAV38847	Primer for amplifi
c 772	10.2	56.7	36	18	AAV93215	Mouse neurotactin
c 773	10.2	56.7	36	19	AAV42028	1,3-Propanediol de
c 774	10.2	56.7	36	19	AAV35770	Synthetic dhaB PC
c 775	10.2	56.7	36	21	AAV35749	Synthetic dhaB gen
c 776	10.2	56.7	36	21	AAV13477	Mouse neurotactin
c 777	10.2	56.7	36	21	AAV13483	Mouse neurotactin
c 778	10.2	56.7	36	21	AAZ89272	Human tissue bindi
c 779	10.2	56.7	36	21	AAZ58933	Murine neurotactin
c 780	10.2	56.7	36	21	AAZ58939	Murine neurotactin
c 781	10.2	56.7	36	21	AAZ38978	Expression vector
c 782	10.2	56.7	36	22	ABA02676	Hinge/Linker oligo
c 783	10.2	56.7	36	22	ABA02677	Hinge/Linker oligo
c 784	10.2	56.7	36	22	AAH42579	PCR primer for DNA
c 785	10.2	56.7	36	22	AAH73759	Human anti-human f
c 786	10.2	56.7	36	22	AAV81998	K. pneumoniae 1,3-
c 787	10.2	56.7	36	22	AAV59261	Murine neurotactin
c 788	10.2	56.7	36	22	AAV59267	Murine neurotactin
c 789	10.2	56.7	36	22	AAV59267	Primer 1 amplifies
c 790	10.2	56.7	36	22	AAV59267	E. blattae 1,3-pro
c 791	10.2	56.7	37	17	AAV16199	Humanised antibody
c 792	10.2	56.7	37	20	AAV86699	Primer p1uHAT6 use
c 793	10.2	56.7	37	20	AAV79803	PCR primer F5110
c 794	10.2	56.7	38	24	AAV99419	Oligonucleotide ca
c 795	10.2	56.7	38	24	ABA97259	Mutagenic primer 1
c 796	10.2	56.7	38	24	ABA97260	Mutagenic primer 2
c 797	10.2	56.7	39	11	AAQ04547	T92 Guess-mer prob
c 798	10.2	56.7	39	22	AAV69803	Human IL1RA1pha po
c 799	10.2	56.7	39	22	AAV69828	Human IL1RA1pha ge
c 800	10.2	56.7	40	21	AAZ96061	polynucleotide seq
c 801	10.2	56.7	40	22	AAV38564	Human C-fos strept
c 802	10.2	56.7	40	22	ABK27881	Corn male reproduc
c 803	10.2	56.7	41	21	AAZ55260	Neisseria species
c 804	10.2	56.7	41	22	AAV6726	Human zinc finger
c 805	10.2	56.7	41	22	AAV6727	Human zinc finger
c 806	10.2	56.7	41	22	ABL50151	Human zinc finger
c 807	10.2	56.7	41	24	ABL50152	Human base mismatch
c 808	10.2	56.7	41	24	AAV18042	Human zinc finger
c 809	10.2	56.7	41	24	AAV18043	Human zinc finger
c 810	10.2	56.7	42	22	AAV82004	Plasmid pDR29 PCR
c 811	10.2	56.7	43	14	AAV54125	tPA insertion sequ
c 812	10.2	56.7	43	14	AAQ54129	tPA insertion sequ

C 813	10.2	56.7	44	19	AAV50985	Maize polymorphic
C 814	10.2	56.7	44	19	AAV50986	Maize polymorphic
C 815	10.2	56.7	44	19	AAV50991	Maize polymorphic
C 816	10.2	56.7	44	19	AAV47808	Maize polymorphic
C 817	10.2	56.7	44	19	AAV47803	Maize polymorphic
C 818	10.2	56.7	44	19	AAV47803	Maize polymorphic
C 819	10.2	56.7	45	14	AAO54128	TPA insertion sequ
C 820	10.2	56.7	45	14	AAO54128	TPA insertion sequ
C 821	10.2	56.7	45	21	AAV37282	Human PRO1491 hybr
C 822	10.2	56.7	45	21	AAV37282	Oligonucleotide IG
C 823	10.2	56.7	45	22	AAV64110	Human prostate cdn
C 824	10.2	56.7	45	22	AAH93874	P703P peptide 4 en
C 825	10.2	56.7	45	24	ABL95481	Human P703P peptid
C 826	10.2	56.7	45	24	ABA89626	Serial analysis of
C 827	10.2	56.7	46	20	AAH91480	T. gondii immunoge
C 828	10.2	56.7	46	22	AAH91480	Human map-related
C 829	10.2	56.7	47	21	AAZ65874	Human map-related
C 830	10.2	56.7	47	21	AAZ65874	Human map-related
C 831	10.2	56.7	47	21	AAZ65874	Human map-related
C 832	10.2	56.7	47	21	AAZ65874	Human map-related
C 833	10.2	56.7	47	21	AAZ65874	Human map-related
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C 835	10.2	56.7	47	21	AAZ65874	Human map-related
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C 838	10.2	56.7	47	21	AAZ65874	Human map-related
C 839	10.2	56.7	47	21	AAZ65874	Human map-related
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C 841	10.2	56.7	47	21	AAZ65874	Human map-related
C 842	10.2	56.7	47	21	AAZ65874	Human map-related
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C 844	10.2	56.7	47	21	AAZ65874	Human map-related
C 845	10.2	56.7	47	21	AAZ65874	Human map-related
C 846	10.2	56.7	47	21	AAZ65874	Human map-related
C 847	10.2	56.7	47	21	AAZ65874	Human map-related
C 848	10.2	56.7	47	21	AAZ65874	Human map-related
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C 850	10.2	56.7	47	21	AAZ65874	Human map-related
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C 852	10.2	56.7	47	21	AAZ65874	Human map-related
C 853	10.2	56.7	47	21	AAZ65874	Human map-related
C 854	10.2	56.7	47	21	AAZ65874	Human map-related
C 855	10.2	56.7	47	21	AAZ65874	Human map-related
C 856	10.2	56.7	47	21	AAZ65874	Human map-related
C 857	10.2	56.7	47	21	AAZ65874	Human map-related
C 858	10.2	56.7	47	21	AAZ65874	Human map-related
C 859	10.2	56.7	47	21	AAZ65874	Human map-related
C 860	10.2	56.7	47	21	AAZ65874	Human map-related
C 861	10.2	56.7	47	21	AAZ65874	Human map-related
C 862	10.2	56.7	47	21	AAZ65874	Human map-related
C 863	10.2	56.7	47	21	AAZ65874	Human map-related
C 864	10.2	56.7	47	21	AAZ65874	Human map-related
C 865	10.2	56.7	47	21	AAZ65874	Human map-related
C 866	10.2	56.7	47	21	AAZ65874	Human map-related
C 867	10.2	56.7	47	21	AAZ65874	Human map-related
C 868	10.2	56.7	47	21	AAZ65874	Human map-related
C 869	10.2	56.7	47	21	AAZ65874	Human map-related
C 870	10.2	56.7	47	21	AAZ65874	Human map-related
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C 873	10.2	56.7	47	21	AAZ65874	Human map-related
C 874	10.2	56.7	47	21	AAZ65874	Human map-related
C 875	10.2	56.7	47	21	AAZ65874	Human map-related
C 876	10.2	56.7	47	21	AAZ65874	Human map-related
C 877	10.2	56.7	47	21	AAZ65874	Human map-related
C 878	10.2	56.7	47	21	AAZ65874	Human map-related
C 879	10.2	56.7	47	21	AAZ65874	Human map-related
C 880	10.2	56.7	47	21	AAZ65874	Human map-related
C 881	10.2	56.7	47	21	AAZ65874	Human map-related
C 882	10.2	56.7	47	21	AAZ65874	Human map-related
C 883	10.2	56.7	47	21	AAZ65874	Human map-related
C 884	10.2	56.7	47	21	AAZ65874	Human map-related
C 885	10.2	56.7	47	21	AAZ65874	Human map-related

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C 959 10 55.6 25 24 ABN14143 Human GDMPL-1 25-m
C 960 10 55.6 25 24 ABN14144 Human GDMPL-1 25-m
C 961 10 55.6 26 26 AAV16265 Dual labeled fluor
C 962 10 55.6 26 22 AAS11183 Human beta-globin
C 963 10 55.6 26 22 AAH45992 Human beta-globin
C 964 10 55.6 26 22 AAF59149 Dual-labeled fluor
C 965 10 55.6 26 22 AAC88349 Probe 262T. Unide
C 966 10 55.6 26 22 AAC88862 HBV polyA sequence
C 967 10 55.6 27 14 AAQ41722 PCR primer to ampl
C 968 10 55.6 27 14 AAQ42192 Encodes C-terminus
C 969 10 55.6 27 14 AAQ38395 M1 primer (1). Sy
C 970 10 55.6 27 19 AAV25373 Primer B1 of the i
C 971 10 55.6 27 22 AAC88881 HBV polyA sequence
C 972 10 55.6 28 16 AAT01011 Modified human lym
C 973 10 55.6 28 16 AAT62489 Infk4-p16 specific
C 974 10 55.6 28 21 AAZ58564 Mouse Infk4-p16 se
C 975 10 55.6 28 22 AAH47826 RT PCR primer 1.
C 976 10 55.6 28 22 AAD03269 Human p53 binding
C 977 10 55.6 29 4 AAN30137 Sequence of DNA fr
C 978 10 55.6 29 14 AAQ52822 HCV target sequenc
C 979 10 55.6 29 14 AAQ52823 HCV target sequenc
C 980 10 55.6 29 15 AAQ82941 Human mutated PIP
C 981 10 55.6 29 16 AAQ79812 Hepatitis C virus
C 982 10 55.6 29 16 AAQ76211 HSV L/ST ORF3. He
C 983 10 55.6 29 18 AAT89682 Probe used in the
C 984 10 55.6 29 20 AAT19522 Integrin alpha 6 s
C 985 10 55.6 29 20 AAZ07634 HCV J1 isolate NS1
C 986 10 55.6 29 20 AAAX26784 PCR primer and pro
C 987 10 55.6 29 20 AAAX00448 Hepatitis C virus
C 988 10 55.6 29 21 AAV92103 Human A-Raf hammer
C 989 10 55.6 29 21 AAF05792 Hammerhead ribozym
C 990 10 55.6 29 21 AAA30369 Plasmid TKH2 PCR
C 991 10 55.6 29 21 AAA03856 Polymorphic fragme
C 992 10 55.6 29 21 AAA04200 Polymorphic fragme
C 993 10 55.6 29 21 AAZ58442 Primer used in pCM
C 994 10 55.6 29 24 AAD26389 3' HBV polymerase
C 995 10 55.6 30 10 AAN92580 Wild type sequence
C 996 10 55.6 30 10 AAN92581 Gln4 mutant sequen
C 997 10 55.6 30 16 AAQ93259 Family 1A bFGF 2'-
C 998 10 55.6 30 18 AAT84861 Human endonuclease
C 999 10 55.6 30 21 AAAS3082 Rat genomic DNA ve
C1000 10 55.6 30 21 AAZ88251 Treponema pallidum
```

ALIGNMENTS

```
RESULT 1
AAS19106
ID AAS19106 standard; DNA; 18 BP.
XX
XX AAS19106;
AC
XX
XX 15-MAR-2002 (first entry)
DT
XX
XX Human p53 coding sequence antisense sequence SEQ ID NO: 35.
DE
XX
XX Antisense; splice region; mRNA splice processing inhibition;
KM splice variant; protein expression inhibition; human; HIV-1; rat; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200183740-A2.
PN
XX
XX 08-NOV-2001.
PD
XX
XX 04-MAY-2001; 2001WO-US14410.
PF
XX 04-MAY-2000; 2000US-202376P.
PR
XX (AVIB-) AVI BIOPHARMA INC.
PA
XX Iversen PL, Hudziak R;
PI
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XX
XX WPI; 2002-066533/09.
DR
XX Splice-region antisense composition and method
PT
XX Claim 18; Page 23; 53pp; English.
PS
XX
XX The present invention relates to antisense compositions targeted to an
CC mRNA sequence for a selected protein, at a region having its 5' end from
CC 1 to about 25 base pairs downstream of a normal splice acceptor junction
CC in the preprocessed mRNA. The antisense compound is RNase-inactive, and
CC is preferably a phosphorodiamidate-linked morpholino oligonucleotide.
CC Such targeting is effective to inhibit natural mRNA splice processing,
CC produce splice variant mRNAs, and inhibit normal expression of the
CC protein. The present sequence is an antisense sequence described in the
CC exemplification of the invention.
XX
SQ Sequence 18 BP; 3 A; 6 C; 7 G; 2 T; 0 other;
Query Match 100.0%; Score 18; DB 24; Length 18;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCGGAAGCAGCTGCG 18
Db 1 CCCGGAAGCAGCTGCG 18
RESULT 2
AAS19107
ID AAS19107 standard; DNA; 36 BP.
XX
XX AAS19107;
AC
XX
XX 15-MAR-2002 (first entry)
DT
XX
XX Human p53 coding sequence antisense sequence SEQ ID NO: 36.
DE
XX
XX Antisense; splice region; mRNA splice processing inhibition;
KM splice variant; protein expression inhibition; human; HIV-1; rat; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200183740-A2.
PN
XX
XX 08-NOV-2001.
PD
XX
XX 04-MAY-2001; 2001WO-US14410.
PF
XX 04-MAY-2000; 2000US-202376P.
PR
XX (AVIB-) AVI BIOPHARMA INC.
PA
XX Iversen PL, Hudziak R;
PI
XX
XX WPI; 2002-066533/09.
DR
XX
XX Splice-region antisense composition and method
PT
XX
XX Claim 37; Page 23; 53pp; English.
PS
XX
XX The present invention relates to antisense compositions targeted to an
CC mRNA sequence for a selected protein, at a region having its 5' end from
CC 1 to about 25 base pairs downstream of a normal splice acceptor junction
CC in the preprocessed mRNA. The antisense compound is RNase-inactive, and
CC is preferably a phosphorodiamidate-linked morpholino oligonucleotide.
CC Such targeting is effective to inhibit natural mRNA splice processing,
CC produce splice variant mRNAs, and inhibit normal expression of the
CC protein. The present sequence is an antisense sequence described in the
CC exemplification of the invention.
XX
SQ Sequence 36 BP; 6 A; 11 C; 12 G; 7 T; 0 other;
```

Query Match 100.0%; Score 18; DB 24; Length 36;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGCAGCTGTGGC 18
 |||||||
 DB 17 CCCGGAAGCAGCTGTGGC 34

RESULT 3
 AAX26511/c
 ID AAX26511 standard; DNA; 37 BP.
 XX
 AC AAX26511;
 XX
 DT 28-MAY-1999 (first entry)
 XX
 DE WO 9909191 SeqID #13.
 XX
 XX Cancer; treatment; vector; recombinase gene; transcription factor;
 KM selective cell killing; gene therapy; primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO9909191-A1.
 XX
 PD 25-FEB-1999.
 XX
 PF 02-JUL-1998; 98WO-JP02993.
 XX
 PR 20-AUG-1997; 97JP-0223651.
 XX
 PA (DNAMV-) DNAMVC RES. INC.
 XX
 PI Hasegawa M, Takeda K, Yokoi H;
 XX
 DK WPI; 1999-181048/15.
 XX
 PT Gene expression specific to cells free from specific transcription
 PT factor with constructed recombinase expression unit after infecting
 PT cells - allowing expression of target gene in gene therapy.
 PT particularly in cancer treatment
 PS Example 1; Page 16; 49pp; Japanese.
 XX
 CC This invention describes a vector containing a recombinase gene which
 CC is controlled by (1) a promoter and action of which is in turn dependent
 CC on a specific transcription factor and (2) a desired gene to be expressed
 CC and two target sequences of the recombinase. Also described in the
 CC invention are (1) a host cell for introduction of the vector and (11) an
 CC in vitro technique in which killing of cells without the specific
 CC transcription factor is selectively performed after the vector is
 CC introduced into a host cell by an in vitro technique. The technique is
 CC used for gene therapy e.g. in cancer treatment. The products of the
 CC invention allow the use of a specific vector specifically and safely,
 CC there is little toxicity.
 CC
 SQ Sequence 37 BP; 7 A; 13 C; 9 G; 8 T; 0 other;

Query Match 100.0%; Score 18; DB 20; Length 37;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGCAGCTGTGGC 18
 |||||||
 DB 30 CCCGGAAGCAGCTGTGGC 13

RESULT 4
 AAG61823/c
 ID AAG61823 standard; DNA; 25 BP.
 XX
 AC AAG61823;

XX
 XX 19-SEP-1994 (first entry)
 DT
 XX Primer for mutant p53 sequence.
 DE
 XX Fragment A: RGC; transcriptional regulator; TR; germ line mutation;
 KM assay; cancer; PCR; amplification; sense; ss.
 XX
 OS Synthetic.
 XX
 PN WO9408049-A.
 XX
 PD 14-APR-1994.
 XX
 XX 28-SEP-1993; 93WO-US09259.
 PF
 XX 01-OCT-1992; 92US-0956696.
 PR
 XX 12-APR-1993; 93US-0046033.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX (SURE-) INST SUISSE RECH EXPERIMENTALE.
 XX
 PI Frebourg T, Friend SH, Iggo R, Ishioka C;
 XX
 DR WPI; 1994-135609/16.
 XX
 PT Assay for mutations in a transcriptional regulator gene - using
 PT cells transfected with the gene and DNA encoding a detectable
 PT protein expressed in response to the gene.
 XX
 PS Example; Page 21; 51pp; English.
 XX
 CC The sequence is that of a sense PCR primer for amplification of a
 CC mutant p53 gene. The PCR prod. can be used in an assay to directly
 CC assess whether a germ-line mutation in a gene which is a trans-
 CC criptional regulator results in the prod. of a non functional gene.
 CC This may be used in screening individuals at risk of cancer or in cancer
 CC prognosis.
 CC See also AAG61818-24.
 CC
 SQ Sequence 25 BP; 4 A; 8 C; 7 G; 6 T; 0 other;

Query Match 83.3%; Score 15; DB 15; Length 25;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGAAGCAGCTGTGGC 18
 |||||||
 DB 25 GGAAGCAGCTGTGGC 11

RESULT 5
 AAC86956/c
 ID AAC86956 standard; DNA; 26 BP.
 XX
 AC AAC86956;
 XX
 DT 02-APR-2001 (first entry)
 XX
 DE PCR primer used to amplify a fragment of DNA encoding p53.
 XX
 XX Antitumor; antiviral; p53; cytotoxic polypeptide; immune response;
 KM tumour; virus-infected cell; proliferative disease; restenosis;
 KM viral infection; hepatitis; herpes; PCR primer; ss.
 XX
 OS Unidentified.
 XX
 PN WO200071078-A2.
 XX
 PD 30-NOV-2000.
 XX
 PF 25-MAY-2000; 2000WO-FR01422.
 XX

PR 25-MAY-1999; 99FR-0006892.
XX
PA (TRGE) TRANSGENE.
XX
PI Erbs P, Jund R;
XX
DR WPI; 2001-061278/07.
XX
PT Composition containing p53 gene and gene for cytotoxin, useful for
PT treating tumours and viral infections, with synergistic activity
XX
PS Example 1, Page 32; 58pp; French.
XX
CC The specification describes a composition for use as antitumor or
CC antiviral agent in mammals. The composition comprises a sequence
CC encoding all or part of p53 and at least one sequence encoding all or
CC part of a cytotoxic polypeptide. These sequences are under control of
CC suitable expression elements. There is a synergistic increase in activity
CC when p53 and the cytotoxic polypeptide are used together, with improved
CC presentation of antigens and/or stimulation of the host's immune cells.
CC The composition is used for the induction and activation of an immune
CC response specific for tumours or virus-infected cells, or inhibition of
CC growth and division (preferably killing) of such cells. The composition
CC is used to treat or prevent tumours (or other proliferative diseases,
CC e.g. restenosis) and viral infections (e.g. caused by hepatitis B or C,
CC herpes of human immune deficiency virus), in humans and animals. PCR
CC primers AAC86956-57 were used to amplify a fragment of DNA encoding p53
CC protein.
XX
SQ Sequence 26 BP; 5 A; 9 C; 7 G; 5 T; 0 other;
XX
Query Match 82.2%; Score 14.8; DB 22; Length 26;
Best Local Similarity 88.9%; Pred. No. 4.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 CCCGAGAGCAGCTGGC 18
DB 22 CCCGAGAGCAATCTGGC 5
XX
RESULT 6
AAL42029
ID AAL42029 standard; DNA; 21 BP.
XX
AC AAL42029;
XX
DT 16-MAY-2002 (first entry)
XX
DE T. reesei endoglucanase III cellulase mutagenic reverse PCR primer H450.
XX
KW Mutagenic PCR; primer; H450; variant endoglucanase III cellulase;
KW variant EgIII cellulase; temperature stress resistant; textile treatment;
KW wood pulp treatment; biomass to glucose reduction; ss;
KW indigo dyed denim stone washing; feed additive.
XX
OS Trichoderma reesei.
OS Synthetic.
XX
PN WO200212463-A2.
XX
PD 14-FEB-2002.
XX
PF 31-JUL-2001; 2001WO-US23960.
XX
PR 04-AUG-2000; 2000US-0632575.
XX
PA (GBV) GENENCOR INT INC.
XX
PI Gualfetti P, Mitchinson C, Ropp TH;
XX
DR WPI; 2002-241749/29.
XX
PT New variant endoglucanase III cellulase useful in treatment of

PT cellulose containing textile, in the reduction of biomass to glucose
PT and as feed additive, has substitution at a residue sensitive to
PT temperature stress
XX
PS Example 1, Page 28; 40pp; English.
XX
CC The invention comprises variant Trichoderma reesei endoglucanase III
CC (EgIII) cellulases which are more resistant to temperature stress than
CC wild type EgIII cellulase. The variant EgIII cellulases of the invention
CC are useful in the treatment of a cellulose containing textile, the
CC treatment of wood pulp, in the reduction of biomass to glucose, stone
CC washing of indigo dyed denim, and as a feed additive. The present
CC nucleotide sequence represents a mutagenic PCR primer used in the
CC production of a variant EgIII cellulase of the invention.
XX
SQ Sequence 21 BP; 3 A; 8 C; 7 G; 3 T; 0 other;
XX
Query Match 73.3%; Score 13.2; DB 24; Length 21;
Best Local Similarity 83.3%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 CCCGAGAGCAGCTGGC 18
DB 4 CTTGGCAGCAGACTGGC 21
XX
RESULT 7
AAL42028/C
ID AAL42028 standard; DNA; 27 BP.
XX
AC AAL42028;
XX
DT 16-MAY-2002 (first entry)
XX
DE T. reesei endoglucanase III cellulase mutagenic forward PCR primer H450.
XX
KW Mutagenic PCR; primer; H450; variant endoglucanase III cellulase;
KW variant EgIII cellulase; temperature stress resistant; textile treatment;
KW wood pulp treatment; biomass to glucose reduction; ss;
KW indigo dyed denim stone washing; feed additive.
XX
OS Trichoderma reesei.
OS Synthetic.
XX
PN WO200212463-A2.
XX
PD 14-FEB-2002.
XX
PF 31-JUL-2001; 2001WO-US23960.
XX
PR 04-AUG-2000; 2000US-0632575.
XX
PA (GBV) GENENCOR INT INC.
XX
PI Gualfetti P, Mitchinson C, Ropp TH;
XX
DR WPI; 2002-241749/29.
XX
PT New variant endoglucanase III cellulase useful in treatment of
PT cellulose containing textile, in the reduction of biomass to glucose
PT and as feed additive, has substitution at a residue sensitive to
PT temperature stress
XX
PS Example 1, Page 28; 40pp; English.
XX
CC The invention comprises variant Trichoderma reesei endoglucanase III
CC (EgIII) cellulases which are more resistant to temperature stress than
CC wild type EgIII cellulase. The variant EgIII cellulases of the invention
CC are useful in the treatment of a cellulose containing textile, the
CC treatment of wood pulp, in the reduction of biomass to glucose, stone
CC washing of indigo dyed denim, and as a feed additive. The present
CC nucleotide sequence represents a mutagenic PCR primer used in the
CC production of a variant EgIII cellulase of the invention.

XX	Sequence	27 BP; 3 A; 10 C; 11 G; 3 T; 0 other;
SO		
XX	Query Match	73.3%; Score 13.2; DB 24; Length 27;
XX	Best Local Similarity	83.3%; Pred. No. 3e+03; Mismatches 3; Indels 0; Gaps 0
XX	Matches 15; Conservative	0;
OY		
	1 CCCGAGCGACGTCTGC 18	
DB	21 CCTGGCAGCGACACTGCC 4	
RESULT 8		
AAT50605/C		
ID	AAT50605 standard; RNA; 18 BP.	
AC		
XX	AAT50605;	
DT	10-MAR-1997 (first entry)	
DE	Human CERP hairpin ribozyme target sequence #280.	
XX		
KW	Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;	
KW	neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;	
KW	reverse cholesterol transport; high density lipoprotein therapy; CERP;	
KW	familial hypercholesterolaemia; dyslipidaemia; hypocalphalipoproteinaemia;	
KW	peripheral vascular disease; hyperbetalipoproteinemia; RCT inhibitor;	
KW	angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;	
LBD, S5.		
XX		
OS	Homo sapiens.	
XX		
PN	M09620279-A1.	
PD	04-JUL-1996.	
XX		
PF	11-DEC-1995; 95MO-US16000.	
PR	23-DEC-1994; 94US-0363240.	
PA	(RIBO-) RIBOZYME PHARM INC.	
PA	(WARN) WARNER LAMBERT CO.	
PX	Bisgater C, Couture L, McSwiggen J, Pape M, Stinchcomb D;	
PX	WPJ: 1996-321852/32.	
XX		
PT	New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA	
PT	- useful for preventing or treating initial development, progression	
PT	or regression of vascular diseases, esp. familial	
PT	hypercholesterolaemia	
PA		
PA	Claim 4; Page 52; 72pp; English.	
CC	AAT50595-T50642 represent target sequences for the human cholesterol	
CC	ester transfer protein (CERT) hairpin ribozymes (see AAT50347-750594).	
CC	CERP is a 74 kb glycoprotein that facilitates neutral lipid transfer	
CC	between plasma lipoproteins. The numbering of the targets refers to the	
CC	position of the cleavage site in full length CERT. The ribozyme then	
CC	binds to 4-6 nucleotides 5' and a variable number 3' of this site. The	
CC	ribozymes are able to cleave mRNA from the gene encoding CERT, thereby	
CC	blocking synthesis and/or expression of the mRNA. By inhibiting CERT,	
CC	the reverse cholesterol transport (RCT) pathway can be inhibited (or	
CC	eliminated) thereby preventing the reduction in size density of the high	
CC	density lipoproteins (HDL), prolonging HDL half life, and therefore	
CC	increasing HDL levels. The ribozymes can be used to treat conditions	
CC	associated with abnormal levels of CERT, specifically atherosclerosis,	
CC	peripheral vascular disease, hyperbetalipoproteinemia, dyslipidaemia,	
CC	familial hypercholesterolaemia, hypocalphalipoproteinemia, vascular	
CC	complications of diabetes, transplant, atherectomy and angioplasty	
CC	restenosis. By inhibiting CERT, the levels of HDL and low density	
CC	lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a	
CC	decrease in LDL levels, and a corresponding increase in HDL levels). The	

CC	mutations can also be used diagnostically to study genetic drift and
CC	mutations in diseased cells, and to detect CERP mRNA. As the ribozymes
CC	target specific regions of the CERP gene, they have low non-specific
CC	activity.
XX	
SQ	Sequence 18 BP; 3 A; 9 C; 4 G; 2 U; 0 other;
	Query Match 71.1%; Score 12.8; DB 17; Length 18;
	Best Local Similarity 87.5%; Pred. No. 4.6e+03;
	Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY	
DJ	2 CCGAAGCAGCTGTCG 17 16 CTGGACGCCGTCTGC 1
RESULT 9	
ID	AAT50701/C
XX	AAT50701 standard; RNA; 18 BP.
XX	
XX	AAT50701:
DN	07-MAR-1997 (first entry)
XX	
DE	Rabbit CERP hairpin ribozyme target sequence #102.
KX	Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
KX	neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
KX	reverse cholesterol transport; high density lipoprotein; therapy; CERP;
KX	familial hypercholesterolaemia; dyslipidaemia; hypolipalphipoproteinaemia;
KX	peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
KX	angioplastic restenosis; low density lipoprotein; diabetes; HDL; rabbit;
KX	LBD; ss.
XX	
OS	Oryctolagus cuniculus.
KX	
FN	W09620279-A1.
PD	04-JUL-1996.
KX	
FF	11-DEC-1995; 95WO-US16000.
KX	
PR	23-DEC-1994; 94US-0363240.
KX	
PA	(RIBO-) RIBOZYME PHARM INC.
PA	(WARN) WARNER LAMBERT CO.
P1	
P1	Bisgaler C, Couture L, McSwigen J, Pape W, Stinchcomb D:
DR	WPI: 1996-321852/32.
XX	
PT	New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
PT	- useful for preventing or treating initial development, progression
PT	or regression of vascular diseases, esp. familial
PT	hypercholesterolaemia
XX	
PS	Claim 4; Page 54; 72pp; English.
XX	
AA	AAT50699-T50754 represent target sequences for the rabbit cholesterol
CC	ester transfer protein (CERT) hairpin ribozymes (see AAT50643-T50698).
CC	CERT is a 74 kb glycoprotein that facilitates neutral lipid transfer
CC	between plasma lipoproteins. The numbering of the targets refers to the
CC	position of the cleavage site in full length CERT. The ribozyme then
CC	binds to 4-6 nucleotides 5' , and a variable number 3' of this site.. The
CC	ribozymes are able to cleave mRNA from the gene encoding CERT, thereby
CC	blocking synthesis and/or expression of the mRNA. By inhibiting CERT,
CC	the reverse cholesterol transport (RCT) pathway can be inhibited (or
CC	eliminated) thereby preventing the reduction in size density of the high
CC	density lipoproteins (HDL), prolonging HDL half life, and therefore
CC	increasing HDL levels. The ribozymes can be used to treat conditions
CC	associated with abnormal levels of CERT, specifically atherosclerosis,
CC	peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
CC	familial hypercholesterolaemia, hypolipalphipoproteinaemia, vascular

CC complications of diabetes, transplant, atherectomy and angioplastic
CC restenosis. By inhibiting CERP, the levels of HDL and low density
CC lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
CC decrease in LDL levels, and a corresponding increase in HDL levels). The
CC ribozymes can also be used diagnostically to study genetic drift and
CC mutations in diseased cells, and to detect CERP mRNA. As the ribozymes
CC target specific regions of the CERP gene, they have low non-specific
CC activity.

SO Sequence 18 BP; 3 A; 8 C; 5 G; 2 U; 0 other;

Query Match 71.1%; Score 12.8; DB 17; Length 18;
Best Local Similarity 87.5%; Pred. No. 4.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CCGGAGGCGACTCTGG 17
| | | | | | | | | | | | | | | | | |
DB 16 CTGGAGGCGCTCTGG 1

RESULT 10
AA092447/c

ID AA092447 standard; DNA; 28 BP.

XX AA092447;

DT 11-JAN-1996 (first entry)

DE CD3 delta chain 3' PCR detection primer.

XX primer; PCR; amplification; natural killer cell; purification; CD3; CD5;
KW antibody; interleukin; proliferation; target cell type; beta-actin;
KW allogenic lymphoblastoid; T-cell receptor; gene expression; ss.

OS Synthetic.

XX US5415874-A.

XX 16-MAY-1995.

XX 31-OCT-1989; 89US-0429353.

XX 31-OCT-1989; 89US-0429353.

PA (STRD) UNIV LELAND STANFORD JUNIOR.

PI Bender JR, Engleman EG, Parol R;

DR WPI: 1995-193394/25.

XX Prodn. of target cell-specific natural killer cells - by selecting
PT natural killer cells based on their adhesion to a selected target
PT cell type and culturing.

PS Example 5; Column 15; 23pp; English.

CC Primers AA092434-49 were used to PCR detect specific messenger RNAs in
CC cultured natural killer (NK) cells. The NK cells are purified by
CC partial purification through a nylon wool column followed by removal
CC of the CD3+ and CD5+ cells by incubating in the presence of bound
CC anti-CD3 and anti-CD5 antibodies. The remaining cells which express
CC the Leu1c+ (CD16) and Leu19 markers are enriched by propagating in a
CC medium containing an agent e.g. interleukin (IL)-2 which promotes
CC proliferation of the NK cells and in the presence of the NK cells'
CC target cell type e.g. allogenic lymphoblastoid cells.
CC Confirmation of the correct NK cell type is carried by PCR amplification
CC of the CD3 and T-cell receptor (TCR) markers alpha, beta, gamma and
CC delta, on reverse transcribed RNA isolated from the NK cells. The
CC primers AA092446-7 target the CD3 gene delta chain.

SO Sequence 28 BP; 6 A; 11 C; 6 G; 5 T; 0 other;

Query Match 71.1%; Score 12.8; DB 16; Length 28;

Best Local Similarity 87.5%; Pred. No. 4.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CCGGAGGCGACTCTGG 17
| | | | | | | | | | | | | | | | | |
DB 26 CTGGAGGCGCTCTGG 11

RESULT 11
AA060604

ID AA060604 standard; DNA; 30 BP.

XX AA060604;

DT 24-JAN-1991 (first entry)

DE N-terminus probe used to isolate p150,95 cell surface adhesion
DE receptor.

XX Rhinovirus; ICAM-1; LFA-1 glycoprotein; multiple sclerosis;
KW ulcerative colitis; transplant rejection; ss.

OS Synthetic.

XX WO9010646-A.

XX 20-SEP-1990.

XX 09-MAR-1990; 90WO-US01257.

XX 09-MAR-1990; 90WO-US01257.

PA (DANA-) DANA FARMER CANCER.

PI Corbi AA, Springer TA;

DR WPI: 1990-304985/40.

XX Treatment of viral esp. rhino-viral infection - by admin. of
PT alpha sub-unit of p150,95 cell surface adhesion receptor. opt.
PT together with a beta chain of CD-18 family

XX Example 1; Page 33; 59pp; English.

CC Probe was used to isolate p150,95 surface adhesion receptor from
CC hairy cell leukemia spleens by Mab affinity chromatography.
CC The isolated receptor prevents viral (particularly rhino-viral) cell-
CC virus adhesion by interacting with ICAM-1. It is useful in treatment
CC of delayed hypersensitivity, multiple sclerosis, transplant
CC rejection, ulcerative colitis etc. Abs against the receptor may be
CC used as antiinflammatory agents.

SO Sequence 30 BP; 7 A; 10 C; 9 G; 4 T; 0 other;

Query Match 71.1%; Score 12.8; DB 11; Length 30;
Best Local Similarity 87.5%; Pred. No. 4.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CCGGAGGCGACTCTG 16
| | | | | | | | | | | | | | | | | |
DB 12 CCGGAGGCGCTCTAG 27

RESULT 12
AAT50604/c

ID AAT50604 standard; RNA; 18 BP.

XX AAT50604;

DT 10-MAR-1997 (first entry)

DE Human CERP hairpin ribozyme target sequence #276.

KM Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
 KM neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
 KM reverse cholesterol transport; high density lipoprotein; therapy; CERP;
 KM familial hypercholesterolemia; dyslipidaemia; hypolipidoproteinaemia;
 KM peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
 KM angioliplastic restenosis; low density lipoprotein; diabetes; HDL; human;
 KM LDL; ss.
 XX
 OS Homo sapiens.
 XX
 PN W09620279-A1.
 XX
 PD 04-JUL-1996.
 XX
 PF 11-DEC-1995; 95WO-US16000.
 XX
 PR 23-DEC-1994; 94US-0363240.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (WARN) WARNER LAMBERT CO.
 XX
 PI Bisgaier C, Couture L, McSwiggen J, Pape M, Stinchcomb D;
 DR WPI; 1996-321852/32.
 XX
 PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
 PT - useful for preventing or treating initial development, progression
 PT or regression of vascular diseases, esp. familial
 PT hypercholesterolaemia
 XX
 PS Claim 4; Page 52; 72pp; English.
 XX
 CC AAT50595-T50642 represent target sequences for the human cholesterol
 CC ester transfer protein (CERP) hairpin ribozymes (see AAT50547-T50599).
 CC CERP is a 74 kd glycoprotein that facilitates neutral lipid transfer
 CC between plasma lipoproteins. The numbering of the targets refers to the
 CC position of the cleavage site in full length CERP. The ribozyme then
 CC binds to 4-6 nucleotides 5', and a variable number 3' of this site. The
 CC ribozymes are able to cleave mRNA from the gene encoding CERP, thereby
 CC blocking synthesis and/or expression of the mRNA. By inhibiting CERP,
 CC the reverse cholesterol transport (RCT) pathway can be inhibited (or
 CC eliminated) thereby preventing the reduction in size density of the high
 CC density lipoproteins (HDL), prolonging HDL half life, and therefore
 CC increasing HDL levels. The ribozymes can be used to treat conditions
 CC associated with abnormal levels of CERP, specifically atherosclerosis,
 CC peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
 CC familial hypercholesterolaemia, hypolipidoproteinaemia, vascular
 CC complications of diabetes, transplant, atherectomy and angioliplastic
 CC restenosis. By inhibiting CERP, the levels of HDL and low density
 CC lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
 CC decrease in LDL levels, and a corresponding increase in HDL levels). The
 CC ribozymes can also be used diagnostically to study genetic drift and
 CC mutations in diseased cells, and to detect CERP mRNA. As the ribozymes
 CC target specific regions of the CERP gene, they have low non-specific
 CC activity.
 CC
 XX
 SQ Sequence 18 BP; 3 A; 8 C; 3 G; 4 U; 0 other;
 XX
 QY Query Match 68.9%; Score 12.4; DB 17; Length 18;
 Db Best Local Similarity 92.9%; Pred. No. 7.3e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 4 GGAAAGCGCTCTGG 17
 18 GGAAAGCGCTCTGG 5
 RESULT 13
 AAT50700/c
 ID AAT50700 standard; RNA: 18 BP.
 AC AAT50700;
 XX

DR 07-MAR-1997 (first entry)
 XX
 DE Rabbit CERP hairpin ribozyme target sequence #98.
 XX
 KM Hairpin ribozyme; cholesterol ester transfer protein; mRNA cleavage;
 KM neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
 KM reverse cholesterol transport; high density lipoprotein; therapy; CERP;
 KM familial hypercholesterolemia; dyslipidaemia; hypolipidoproteinaemia;
 KM peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
 KM angioliplastic restenosis; low density lipoprotein; diabetes; HDL; rabbit;
 KM LDL; ss.
 XX
 OS Oryctolagus cuniculus.
 XX
 PN W09620279-A1.
 XX
 PD 04-JUL-1996.
 XX
 PF 11-DEC-1995; 95WO-US16000.
 XX
 PR 23-DEC-1994; 94US-0363240.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (WARN) WARNER LAMBERT CO.
 XX
 PI Bisgaier C, Couture L, McSwiggen J, Pape M, Stinchcomb D;
 DR WPI; 1996-321852/32.
 XX
 PT New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA
 PT - useful for preventing or treating initial development, progression
 PT or regression of vascular diseases, esp. familial
 PT hypercholesterolaemia
 XX
 PS Claim 4; Page 54; 72pp; English.
 XX
 CC AAT50699-T50754 represent target sequences for the rabbit cholesterol
 CC ester transfer protein (CERP) hairpin ribozymes (see AAT50643-T50698).
 CC CERP is a 74 kd glycoprotein that facilitates neutral lipid transfer
 CC between plasma lipoproteins. The numbering of the targets refers to the
 CC position of the cleavage site in full length CERP. The ribozyme then
 CC binds to 4-6 nucleotides 5', and a variable number 3' of this site. The
 CC ribozymes are able to cleave mRNA from the gene encoding CERP, thereby
 CC blocking synthesis and/or expression of the mRNA. By inhibiting CERP,
 CC the reverse cholesterol transport (RCT) pathway can be inhibited (or
 CC eliminated) thereby preventing the reduction in size density of the high
 CC density lipoproteins (HDL), prolonging HDL half life, and therefore
 CC increasing HDL levels. The ribozymes can be used to treat conditions
 CC associated with abnormal levels of CERP, specifically atherosclerosis,
 CC peripheral vascular disease, hyperbetalipoproteinaemia, dyslipidaemia,
 CC familial hypercholesterolemia, hypolipidoproteinaemia, vascular
 CC complications of diabetes, transplant, atherectomy and angioliplastic
 CC restenosis. By inhibiting CERP, the levels of HDL and low density
 CC lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a
 CC decrease in LDL levels, and a corresponding increase in HDL levels). The
 CC ribozymes can also be used diagnostically to study genetic drift and
 CC mutations in diseased cells, and to detect CERP mRNA. As the ribozymes
 CC target specific regions of the CERP gene, they have low non-specific
 CC activity.
 CC
 XX
 SQ Sequence 18 BP; 2 A; 7 C; 5 G; 4 U; 0 other;
 XX
 QY Query Match 68.9%; Score 12.4; DB 17; Length 18;
 Db Best Local Similarity 92.9%; Pred. No. 7.3e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 4 GGAAAGCGCTCTGG 17
 18 GGAAAGCGCTCTGG 5
 RESULT 14
 AAA87923/c

```

ID  AAA87923 standard; DNA; 26 BP.
XX
OS  AAA87923;
AC  AAA87923;
XX
XX  07-DEC-2000 (first entry)
DE  Human beta-3-adrenergic receptor promoter PCR primer SEQ ID NO:22.
XX
XX  Human: beta-3-adrenergic receptor; beta-3-AR; transcription; promoter;
KM  regulation; identification; trans-activating factor; drug screening;
KW  gene expression regulation; obesity; type II diabetes; PCR primer; ss.
XX
OS  Homo sapiens.
XX
XX  WO200044901-A1.
XX
XX  03-AUG-2000.
XX
XX  01-FEB-2000; 2000WO-US02632.
XX
XX  01-FEB-1999; 99US-0243335.
XX
XX  (AMHP ) AMERICAN HOME PROD CORP.
XX
XX  Susulic VS, Duzic E;
XX
XX  WPI: 2000-482973/42.
XX
XX  New isolated nucleic acid useful for screening assays to identify
PT  compounds capable of regulating beta3-AR (adrenergic receptor)
PT  expression, is composed of three regulatory segments
XX
XX  Example 1; Page 34; 88pp; English.
XX
XX  The present invention describes a core nucleotide sequence from the
CC  B segment of the human beta-3-adrenergic receptor (beta-3-AR) regulatory
CC  region. The core nucleotide sequence binds to a B-segment-binding
CC  trans-activating factor. Recombinant vectors under control of the
CC  transcription regulation region comprising nucleotide sequences
CC  containing the core nucleotide sequence from the B segment of the human
CC  beta-3-AR regulatory region provide a substrate for high throughput
CC  assays, particularly reporter gene assays to identify compounds capable
CC  of increasing or decreasing the level of expression of beta-3-AR. The
CC  nucleotide sequences can be used for regulating gene expression and for
CC  drug screening. It is envisaged that beta-3-AR stimulation may have
CC  beneficial effects in the treatment of obesity and type II diabetes.
CC  The present sequence represents a PCR primer for the human beta-3-AR
CC  promoter, which is used in an example from the present invention.
XX
XX  Sequence 26 BP; 3 A; 11 C; 5 G; 7 T; 0 other;
XX
XX  Query Match 68.9%; Score 12.4; DB 21; Length 26;
XX  Best Local Similarity 92.9%; Pred. No. 7.4e+03;
XX  Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX  5 GAAGGCACTCTGGC 18
XX  ||||| |||||
XX  24 GAAGGCACTCTGGC 11
XX
XX  RESULT 15
XX  ABR33460/c
XX  ID  ABR33460 standard; DNA; 17 BP.
XX
XX  ABR33460;
XX
XX  23-APR-2002 (first entry)
XX
XX  Human TNF-receptor II 3'UNT nt 1663 (G/A) reverse PCR primer.
XX
XX  Human: anti-tumour necrosis factor receptor II; TNF receptor II;
XX  TNF receptor I; infliximab therapy; Crohn's disease; malignant disorder;
XX  inflammatory disorder; chronic disease; receptor; primer; ss.
XX

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XX
XX  Homo sapiens.
OS
XX  EPI172444-A1.
XX
XX  16-JAN-2002.
XX
XX  10-JUL-2000; 2000EP-0114786.
XX
XX  10-JUL-2000; 2000EP-0114786.
XX
XX  (CONA-) CONARIS RES INST GMBH.
XX
XX  Schreiber S, Hampe J, Mascheretti S;
XX
XX  WPI: 2002-156651/21.
XX
XX  Detecting non-responders to anti-human necrosis factor therapy,
PT  comprises testing an individual for homozygosity for a single
PT  nucleotide polymorphism in the gene coding for the tumour necrosis
PT  factor receptor II
XX
XX  Disclosure; Page 7; 45pp; English.
XX
XX  The present invention relates to a method for detecting non-responders
CC  to anti-tumour necrosis factor (TNF) therapy. The method involves testing
CC  an individual for homozygosity for at least one single nucleotide
CC  polymorphism (SNP) in the gene coding for TNF receptor II, which is
CC  located on chromosome 1p36. Two novel SNPs, one in exon 2 (position 168
CC  A/G) and one in exon 6 (position 587 T/G) which result in Lys56Lys and
CC  Met196Arg respectively, are also described. The method of the invention
CC  is useful for detecting non-responders to anti-TNF therapy such as
CC  infliximab therapy, or therapy of Crohn's disease. The genes containing
CC  the 2 novel polymorphisms are useful for diagnostic purposes in
CC  inflammatory, malignant or other chronic diseases. The present sequence
CC  represents a Taqman primer used in the methods of the present invention.
XX
XX  Sequence 17 BP; 3 A; 8 C; 4 G; 2 T; 0 other;
XX
XX  Query Match 67.8%; Score 12.2; DB 24; Length 17;
XX  Best Local Similarity 82.4%; Pred. No. 9.2e+03;
XX  Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX  1 CCCGGAAGCAGCTCTGG 17
XX  ||||| |||||
XX  17 CTCGGAAGCAGCTCTGG 1
XX
XX  RESULT 16
XX  AAQ50876
XX  ID  AAQ50876 standard; DNA; 20 BP.
XX
XX  AAQ50876;
XX
XX  13-MAY-1994 (first entry)
XX
XX  HSV2 primer.
XX
XX  HSV: HSV2; herpes simplex virus; detection; body fluid; probe;
XX  biotin; ss.
XX
XX  Synthetic.
XX
XX  JP05260999-A.
XX
XX  12-OCT-1993.
XX
XX  16-MAR-1992; 92JP-0090268.
XX
XX  16-MAR-1992; 92JP-0090268.
XX
XX  (IATR ) IATRON LAB INC.
XX

```

```

DR      WPI: 1993-356464/45.
XX
PT      Specific detection of herpes simplex virus 2 - using combination
PT      of two primers with sequences from specified sequences of DNA
XX
PS      Disclosure; Page 6; 8pp; Japanese.
XX
CC      The primers are used for the rapid and specific detection of
CC      herpes simplex virus 2 (HSV2) in body fluids
CC      pharyngeal secretion and cerebrospinal fluid).
XX
SQ      Sequence 20 BP; 3 A; 7 C; 10 G; 0 U; 0 other;
XX
Query Match
Best Local Similarity 67.8%; Score 12.2; DB 14; Length 20;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0
XX
DY      1 CCCGGAAGCGACTCTGG 17
1 CCCGGAAGCGACTCTGG 17

```

ID	19	CCAGGAAGGAGCTCG	3
RESULT 18			
ABAO2225/C			
ID	ABAO2225	standard; DNA: 20 bp.	
AC			
XX	ABAO2225;		
XX			
XX	12-FEB-2002	(first entry)	
XX			
XX	Human/mouse C/EBP phosphorothioate antisense oligonucleotide, SEQ ID:3.3		
XX			
XX	Human; C/EBP alpha; CCAAT/enhancer-binding protein alpha; CEBPA;		
XX	transcription factor; tissue development; cellular function;		
XX	proliferation; differentiation; adipocyte; energy metabolism;		
XX	chondrogenesis; ovulation; follicular development;		
XX	hepatic steroid-induced cell cycle arrest; G1/S promoter regulation;		
XX	hormonal metabolic regulation; granulocyte development; cancer;		
XX	tumour formation; infection; inflammation; expression inhibition;		
XX	antisense therapy; quantitative real-time PCR primer; ss.		
OS	Homo sapiens.		
XX	Mus musculus.		
XX			
XX	Key		
XX	modified_base	Location/Qualifiers	
XX		1..20	
XX		/*tag- a	
XX		/mod_base- OTHER	
XX		/note= "Phosphorothioate linkages"	
XX	modified_base	1..5	
XX		/*tag- b	
XX		/mod_base- OTHER	
XX		/note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE	
XX	modified_base	16..20	
XX		cytosines are 5-methylcytosine"	
XX		/*tag- c	
XX		/mod_base- OTHER	
XX		/note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE	
XX		cytosines are 5-methylcytosine"	
XX	US6306655-B1.		
XX			
XX	23-OCT-2001.		
XX			
XX	13-JUN-2000; 2000US-0593589.		
XX			
XX	13-JUN-2000; 2000US-0593589.		
XX			
XX	(ISIS-) ISIS PHARM INC.		
XX			
XX	Monia BP, Butler MM, Wyatt J;		
XX			
XX	WPI; 2002-040202/05.		
XX			
XX	New antisense oligonucleotides for modulating the expression of		
XX	CCAAT/enhancer-binding proteins alpha, particularly useful for		
XX	preventing, delaying or treating infection, inflammation or tumor		
XX	formation		
XX			
XX	Claim 1: Column 42; 44pp; English.		
XX			
XX	Sequences ABA02205-ABA02282 represent antisense oligonucleotides		
XX	targeted to the human CCAAT/enhancer-binding protein alpha		
XX	(C/EBP alpha) gene, which inhibit its expression. The antisense		
XX	oligonucleotides were designed to target different regions of		
XX	the human C/EBP alpha RNA, and were analysed for their effect		
XX	on C/EBP alpha mRNA levels by quantitative real-time PCR. A similar		
XX	investigation on mouse C/EBP alpha expression was performed using a		
XX	subset of the antisense oligonucleotides that were capable of hybridising		
XX	to mouse C/EBP alpha mRNA. The C/EBP family of proteins are a family of		
XX	transcription factors which regulate the expression of wide range of		

CC genes that control normal tissue development, cellular function,
 CC cellular proliferation and functional differentiation. C/EBP alpha (also
 CC known as CEBPA) is primarily found in tissues involved in energy
 CC metabolism which have a capacity to metabolise lipids, cholesterol and
 CC other sterols. It is thought to be involved in the regulation of
 CC adipocyte and chondrogenic differentiation, and is also involved in
 CC follicular development and ovulation, steroid-induced cell cycle arrest
 CC in the liver, in controlling glucose transporter GLUT2 promoter activity,
 CC in the hormonal regulation of metabolism, and in granulocyte development.
 CC The oligonucleotides of the invention are useful for diagnosis,
 CC prevention and treatment of conditions associated with C/EBP expression,
 CC such as cancer, tumour formation, infection, or inflammation.

XX
 SQ Sequence 20 BP; 3 A; 8 C; 6 G; 3 T; 0 other;

Query Match 67.8%; Score 12.2; DB 24; Length 20;
 Best Local Similarity 82.4%; Pred. No. 9.2e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CCGGAGAGCAGCTGTG 17
 |||||
 DB 17 CCGGAGAGCAGCTGTG 1

RESULT 19

ABL53569
 ID ABL53569 standard; DNA; 24 BP.

AC ABL53569;

DT 10-JUN-2002 (first entry)

DE Human calcitonin 15.18 PCR primer #1.

KW Calcitonin 15.18; human; foetal abnormality; autoimmune disease;
 KM tumour; ageing; immunomodulator; cytostatic; gene therapy; PCR;
 KM primer; ss.

OS Homo sapiens.

PN WO200220778-A1.

PD 14-MAR-2002.

PF 02-JUL-2001; 2001WO-CN01124.

PR 07-JUL-2000; 2000CN-0117059.

PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.

PI Mao Y, Xie Y;

DR WPI; 2002-269626/31.

PT Human calcitonin 15.18 and encoding polynucleotide, used in diagnosis
 PT and treatment of malignant tumors, hemopathy, human immunodeficiency
 PT virus infection, immunological diseases and inflammation -

PS Example 2; Page 11; 32pp; Chinese.

CC The present invention relates to human calcitonin 15.18 (see
 CC ABL53569). The calcitonin protein and its coding sequence are
 CC useful for the diagnosis and treatment of foetal abnormality,
 CC autoimmune disease, tumours, and for the study of human ageing.
 CC The present sequence is a PCR primer, which was used in an example
 CC from the invention.

SQ Sequence 24 BP; 3 A; 7 C; 12 G; 2 T; 0 other;

Query Match 67.8%; Score 12.2; DB 24; Length 24;
 Best Local Similarity 82.4%; Pred. No. 9.3e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 CCGGAGAGCAGCTGTGC 18
 |||||
 DB 6 CAGGAGAGCAGCTGTGC 22

RESULT 20

AAV08917
 ID AAV08917 standard; DNA; 26 BP.

AC AAV08917;

DT 26-FEB-1999 (first entry)

DE PCR primer for SIV gag gene.

KW PCR primer; SIV; gp120 gene; gag gene; chimeric virus; SIV-HIV virus;
 KM AIDS-associated symptom; HIV; env protein; ss.

OS Synthetic.

PN US5849994-A.

PD 15-DEC-1998.

PF 16-MAY-1995; 95US-0442010.

PR 16-MAY-1995; 95US-0442010.

PA (UNIV) UNIV KANSAS MEDICAL CENT.

PI Narayan O;

DR WPI; 1999-069838/06.

PT Chimeric SIV-HIV virus - for producing AIDS symptoms in macaque
 PT monkeys

PS Example; Column 15; 13pp; English.

CC This sequence represents a PCR primer for the simian immunodeficiency
 CC virus (SIV) gag gene. The amplified sequence can be used in the
 CC chimeric virus of the invention. The chimeric virus is a chimeric SIV-HIV
 CC virus (SHIV) that infects macaque monkeys and causes them to develop
 CC AIDS-associated symptoms within 32 weeks, where the virus is generated by
 CC at least two passages of a SHIV containing DNA encoding HIV env protein
 CC through macaque bone marrow in vivo. The monkeys are useful as an animal
 CC model for HIV-1-induced disease.

SQ Sequence 26 BP; 8 A; 5 C; 11 G; 2 T; 0 other;

Query Match 67.8%; Score 12.2; DB 20; Length 26;
 Best Local Similarity 82.4%; Pred. No. 9.3e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CCGGAGAGCAGCTGTG 17
 |||||
 DB 1 CCGGAGAGCAGCTGTG 17

RESULT 21

AAQ87560/C
 ID AAQ87560 standard; DNA; 32 BP.

AC AAQ87560;

DT 04-JAN-1996 (first entry)

DE HTLVIII amplification primer XHOM.

KW Human immunodeficiency virus; asymmetric; hammerhead; ribozyme; helix I;
 KM helix II; helix III; loop 2; cleavage site; amplification; PCR; primer;
 KM motif; construct; pathogen; retrovirus infection; ss.

Tue Dec 3 12:34:36 2002

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Page 17

```
XX OS Synthetic.
XX FT Key
XX FT misc_binding
XX FT /tag=^a
XX FT /note="binds to HTLVIII sequence"
XX W09510608-A1.
XX PD 20-APR-1995.
XX PF 15-OCT-1993; 93WO-EP02853.
XX PR 15-OCT-1993; 93WO-EP02853.
XX PA (DKFZ-) DKFZ DEUT KREBSFORSCHUNGSZENTRUM STIFTUN.
XX PA (FORT-) FORT FOUND RES & TECHNOLOGY HELLAS.
XX PI Homann M, Sczakiel G, Tabler M;
XX DR WPI: 1995-161795/21.
XX FT Asymmetric hammerhead ribozyme(s) and constructs - having high
XX FT catalytic activity and improved specificity for inactivating target
XX FT RNA e.g. in unwanted endogenous genes or pathogens
XX Example 2; Fig 7; 72pp; English.
XX A primer used in conjunction with primer AR6B (AA087556) to generate an
XX CC inactive asymmetric ribozyme which lacks a nucleotide at position 12 of
XX CC the catalytic domain. The ribozyme is used as a control at position 12 of
XX CC the catalytic domain. The ribozyme alpha-Y-R2195 (AA087567). The
XX CC encoded region provides the Helix III and part of the Helix II of the
XX CC RNA. The construct encodes the asymmetric ribozyme GUC in the target
XX CC (AA087567) rich cleaves the HTLVIII RNA sequence AA087566. The
XX CC asymmetric ribozymes generated by transfection of the constructs can be
XX CC pathogenic RNA e.g. in viral or retroviral infections such as HIV
XX SQ Sequence 32 BP; 6 A; 9 C; 10 G; 7 T; 0 other;
XX Query Match 67.8%; Score 12.2; DB 16; Length 32;
XX Best Local Similarity 82.4%; Pred. No. 9.4e+03;
XX Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX QY 2 CCGGAGCGACGCTGCGC 18
XX DB 25 CCTCAAGCGACGTTGGC 9
XX RESULT 22
XX ID AA089758/c
XX AC AA089758 standard; DNA; 32 BP.
XX XX
XX DT 08-FEB-1996 (first entry)
XX DE Primer XHOM to amplify HTLV-III bases 5819-6382.
XX DE Hammerhead ribozyme; catalytic site; helix; asymmetric; specificity; HIV;
XX KW Prokaryote; eukaryote; fruit ripening gene; protective agent; fungus;
XX KW Virus; insect pathogen; fruit ripening gene; protective agent; fungus;
XX OS Polymerase chain reaction; primer; amplification; ss.
XX FT Key
XX FT misc_binding 14..32
XX FT Location/Qualifiers
```

```
XX FT /tag=^a
XX FT /note="binds to template DNA pAR6 (AA089755)"
XX W09510609-A1.
XX PD 20-APR-1995.
XX PF 14-OCT-1994; 94WO-EP03391.
XX PR 15-OCT-1993; 93WO-EP02853.
XX PA (DKFZ-) DKFZ DEUT KREBSFORSCHUNGSZENTRUM STIFTUN.
XX PA (FORT-) FORT FOUND RES & TECHNOLOGY HELLAS.
XX PI Homann M, Sczakiel G, Tabler M;
XX DR WPI: 1995-161796/21.
XX FT Asymmetric hammerhead ribozymes - and corresp. coding constructs,
XX FT useful for inactivation or suppression of target genes, e.g. in
XX FT pathogens or during fruit ripening
XX Example 2; Fig 7b; 83pp; English.
XX Primers AA089756-8 were used to amplify bases 5845-6049 of the human
XX CC T-cell lymphotropic virus III (HTLV-III) in plasmid pAR6
XX CC (AA089755). The amplified fragment was used to replace the helix I
XX CC sequence of construct pBS29-R2195 (AA089745). This primer helix I
XX CC is a non-functional control. The wild type from the catalytic domain
XX CC and cleaves the ribozyme (alpha)Y-R2195 (AA089754), which targets
XX CC sequence (AA089762). The construct was used to generate a ribozyme
XX CC and a shortened helix I sequence. The ribozyme and a hammerhead ribozyme
XX CC asymmetric in that they contain serially deleted helix I sequences (see
XX CC AA089772-80 for other examples). By interchanging the helix I and III
XX CC sequences, the specificity of the ribozymes can be altered e.g. they can
XX CC be used to inactivate or suppress target RNAs in prokaryote or eukaryote
XX CC cells such as suppressing certain fruit ripening genes or as protective
XX CC agents against fungal, viral or insect pathogens in transgenic plants or
XX CC transformed organisms.
XX SQ Sequence 32 BP; 6 A; 9 C; 10 G; 7 T; 0 other;
XX Query Match 67.8%; Score 12.2; DB 16; Length 32;
XX Best Local Similarity 82.4%; Pred. No. 9.4e+03;
XX Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX QY 2 CCGGAGCGACGCTGCGC 18
XX DB 25 CCTCAAGCGACGTTGGC 9
XX RESULT 23
XX ID AA211413
XX AC AA211413 standard; DNA; 33 BP.
XX XX
XX DT 26-OCT-1999 (first entry)
XX DE Oligo for mutating natural splice donor site within a packaging signal.
XX DE Retroviral vector; functional splice donor site; hybrid viral vector;
XX KW functional splice acceptor site; in vivo gene delivery; therapeutic;
XX KW lentiviral vector; modified hematopoietic stem cell; MHC; tumor; MLC;
XX OS Ischemia; hypoxia response element; HRE; hypoxia; PCR primer; ss.
XX FT Key
XX FT misc_binding W09515684-A2.
XX FT Location/Qualifiers
```

PD 01-APR-1999.
XX
XX 23-SEP-1998; 98WO-GB02885.
XX
XX 25-SEP-1997; 97GB-0020465.
PR 23-SEP-1997; 97GB-0020216.
XX
XX (OXFO-) OXFORD BIOMEDICA UK LTD.
PI Bebbington C, Binley KM, Lewis C, Naylor S;
XX WPI, 1999-263482/22.
XX
XX New retroviral vectors, for, e.g. delivering nucleotide sequences to
PT solid tumor sites
XX
XX
XX Example 6; Page 177; 288pp; English.
XX
XX The invention relates to a retroviral vector (RVV) comprising a
CC functional splice donor site (FSDS) and a functional splice acceptor site
CC (FSAS) where: (i) the FSDS and the FSAS flank a first nucleotide sequence
CC of interest (NOI); (ii) the FSDS is upstream of the FSAS; (iii) the RVV
CC is derived from a retroviral pro-vector; (iv) the retroviral pro-vector
CC comprises a first nucleotide sequence (NS) capable of yielding the FSDS
CC and a second NS capable of yielding the FSAS; and (v) the first NS is
CC downstream of the second NS, such that the RVV is formed as a result of
CC reverse transcription of the retroviral pro-vector. A hybrid viral vector
CC (VV) system for in vivo gene delivery, which system comprises a primary
CC VV which encodes a secondary VV, the primary vector capable of infecting
CC a first target cell and of expressing the secondary VV, which secondary
CC vector is capable of transducing a secondary target cell, where the
CC primary vector is obtainable from or is based on an adenoviral vector and
CC the secondary VV is obtainable from or is based on an RVV preferably a
CC lentiviral vector (LVV) is also provided. The systems can be used for
CC delivering NOIs to one or more target sites. The NOIs may encode
CC therapeutic or diagnostic agents. The methods are used particularly for
CC producing modified hematopoietic stem cells (HMSCs) to deliver NOIs to
CC sites such as solid tumours, which are characterised by ischemia, such as
CC hypoxia or low glucose concentration. The system permits the stable
CC expression of NOIs in targeted cells, e.g. rapidly dividing cells.
XX
SQ Sequence 33 BP; 10 A; 11 C; 9 G; 3 T; 0 other;
Query Match 67.8%; Score 12.2; DB 20; Length 33;
Best Local Similarity 82.4%; Pred. No. 9.4e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 2 CCGGAAGGCACTGTGGC 18
 |||||
DB 7 CCGGAGGCAAGCTGGC 23
RESULT 24
AAA74925
ID AAA74925 standard; DNA; 36 BP.
AC AAA74925;
XX
XX 02-JAN-2001 (first entry)
XX
XX Nucleotide sequence of a substrate nucleic acid.
XX
XX Nucleic acid labelling; signal domain; substrate; signal template; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FT misc_feature 31..36
XX FT /*tag= a
XX FT /note= "template hybridisation domain"
XX
XX WO200046232-A1.

PD 10-AUG-2000.
XX
XX 04-FEB-2000; 2000WO-US02897.
XX
XX 05-FEB-1999; 99US-0118721.
XX
XX (INTE-) INTEGRATED DNA TECHNOLOGIES INC.
XX
XX Behlke MA, Devor EJ, James SA, Walder JA;
PI WPI, 2000-514944/46.
XX
XX
XX Labeling nucleic acid for detecting target nucleic acids, comprises
PT hybridising first and second nucleic acids with DNA polymerase and
PT labelled nucleotide, to create single domain hybridisable with signal
PT template domain
XX
XX
XX Example 3; Page 35; 70pp; English.
XX
XX The specification describes a method for labelling a nucleic acid
CC molecule. The method comprises hybridising a first nucleic acid to
CC a second nucleic acid, and extending the second nucleic acid with a
CC DNA polymerase in the presence of a labelled nucleotide, to create
CC a signal domain having a sequence which shows complementarity towards
CC and is hybridisable to a signal template domain of the first nucleic
CC acid, so that the second nucleic acid is labelled. The first nucleic
CC acid comprises a substrate hybridisation domain of 5-20 nucleotides
CC and a signal template domain of 5-100, from 3' to 5'. The second
CC nucleic acid comprises a template hybridisation domain of 5-20 which
CC is not detectably labelled, and complementary to and hybridisable
CC with the substrate hybridisation domain of the first nucleic acid,
CC and a target binding domain which is not detectably labelled. The
CC method is useful for labelling nucleic acids, so that a labelled complex
CC of nucleic acid useful as probe is formed. The present sequence
CC represents a substrate nucleic acid of the invention.
XX
SQ Sequence 36 BP; 8 A; 8 C; 17 G; 3 T; 0 other;
Query Match 67.8%; Score 12.2; DB 21; Length 36;
Best Local Similarity 82.4%; Pred. No. 9.5e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 CCGGAGGCAAGCTGG 17
 |||||
DB 3 CCGGAGGCAAGCTGG 19
RESULT 25
AAA74926
ID AAA74926 standard; DNA; 36 BP.
AC AAA74926;
XX
XX 02-JAN-2001 (first entry)
XX
XX Nucleotide sequence of a substrate nucleic acid.
XX
XX Nucleic acid labelling; signal domain; substrate; signal template; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FT modified_base 1
XX FT /*tag= a
XX FT /note= "labelled with 32P"
XX
XX WO200046232-A1.
XX
XX 10-AUG-2000.
XX
XX 04-FEB-2000; 2000WO-US02897.
XX
XX 05-FEB-1999; 99US-0118721.


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XX PA (INTE-) INTEGRATED DNA TECHNOLOGIES INC.
XX PI Behlke MA, Devor EJ, James SA, Walder JA;
XX DR WPI; 2000-514944/46.
XX
PT Labeling nucleic acid for detecting target nucleic acids, comprises
PT hybridizing first and second nucleic acids with DNA polymerase and
PT labelled nucleotide, to create single domain hybridisable with signal
PT template domain -
XX
PS Example 4; Page 39; 70pp; English.
XX
CC The specification describes a method for labelling a nucleic acid
CC molecule. The method comprises hybridising a first nucleic acid to
CC a second nucleic acid, and extending the second nucleic acid with a
CC DNA polymerase in the presence of a labelled nucleotide, to create
CC a signal domain having a sequence which shows complementarity towards
CC and is hybridisable to a signal template domain of the first nucleic
CC acid, so that the second nucleic acid is labelled. The first nucleic
CC acid comprises a substrate hybridisation domain of 3-20 nucleotides
CC and a signal template domain of 3-100, from 3' to 5'. The second
CC nucleic acid comprises a template hybridisation domain of 5-20 which
CC is not detectably labelled, and complementary to and hybridisable
CC with the substrate hybridisation domain of the first nucleic acid,
CC and a target binding domain which is not detectably labelled. The
CC method is useful for labelling nucleic acids, so that a labelled complex
CC of nucleic acid useful as probe is formed. The present sequence
CC represents a substrate nucleic acid of the invention.
XX
SQ Sequence 36 BP; 8 A; 8 C; 17 G; 3 T; 0 other;
XX
Query Match 67.8%; Score 12.2; DB 21; Length 36;
Best Local Similarity 82.4%; Pred. No. 9.5e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1 CCCGAGAGCAGCTCG 17
Db 3 CCAGGAGGAGGAGGCTCG 19
XX
RESULT 26
AAAT4927
ID AAAT4927 standard; DNA; 46 BP.
XX
AC AAAT4927;
XX
DT 02-JAN-2001 (first entry)
XX
DE Nucleotide sequence of a substrate nucleic acid.
XX
KM Nucleic acid labelling; signal domain; substrate; signal template; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /note= "labelled with 32P"
XX
PN WO200046232-A1.
XX
PD 10-AUG-2000.
XX
PE 04-FEB-2000; 2000WO-US02897.
XX
PR 05-FEB-1999; 99US-0118721.
XX
PA (INTE-) INTEGRATED DNA TECHNOLOGIES INC.
XX
PI Behlke MA, Devor EJ, James SA, Walder JA;
XX

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DR WPI; 2000-514944/46.
XX
PT Labeling nucleic acid for detecting target nucleic acids, comprises
PT hybridizing first and second nucleic acids with DNA polymerase and
PT labelled nucleotide, to create single domain hybridisable with signal
PT template domain -
XX
PS Example 4; Page 39; 70pp; English.
XX
CC The specification describes a method for labelling a nucleic acid
CC molecule. The method comprises hybridising a first nucleic acid to
CC a second nucleic acid, and extending the second nucleic acid with a
CC DNA polymerase in the presence of a labelled nucleotide, to create
CC a signal domain having a sequence which shows complementarity towards
CC and is hybridisable to a signal template domain of the first nucleic
CC acid, so that the second nucleic acid is labelled. The first nucleic
CC acid comprises a substrate hybridisation domain of 3-20 nucleotides
CC and a signal template domain of 3-100, from 3' to 5'. The second
CC nucleic acid comprises a template hybridisation domain of 5-20 which
CC is not detectably labelled, and complementary to and hybridisable
CC with the substrate hybridisation domain of the first nucleic acid,
CC and a target binding domain which is not detectably labelled. The
CC method is useful for labelling nucleic acids, so that a labelled complex
CC of nucleic acid useful as probe is formed. The present sequence
CC represents a substrate nucleic acid of the invention.
XX
SQ Sequence 46 BP; 18 A; 8 C; 17 G; 3 T; 0 other;
XX
Query Match 67.8%; Score 12.2; DB 21; Length 46;
Best Local Similarity 82.4%; Pred. No. 9.6e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1 CCCGAGAGCAGCTCG 17
Db 3 CCAGGAGGAGGAGGCTCG 19
XX
RESULT 27
AAL27830
ID AAL27830 standard; DNA; 50 BP.
XX
AC AAL27830;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #1038.
XX
KM Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KM neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;
KM amyloid protein; angiotensin; apoptosis related protein; cadherin;
KM cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KM complement related protein; cytochrome; kinase; cytokine; interferon;
KM interleukin; G-protein coupled receptor; thioesterase; inflammation;
KM multifactorial disease; autoimmune disease; infection;
KM nervous system disease; ss.
XX
OS Homo sapiens.
XX
FH Homo sapiens.
FT WO200147944-A2.
FT 05-JUL-2001.
XX
PD 28-DEC-2000; 2000WO-US35498.
XX
PE 28-DEC-1999; 99US-0173419.
XX
PR 27-DEC-2000; 2000US-0173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shinkets RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX

```

PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
CC oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections -
XX
XX
PS Claim 1; Page 1676; 4143bp; English.
XX
XX The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms.
XX
XX Sequence 50 BP; 9 A; 10 C; 21 G; 10 T; 0 other;
SQ
Query Match 67.8%; Score 12.2; DB 22; Length 50;
Best Local Similarity 82.4%; Pred. No. 9.6e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0
QY 2 CCGAAGGACGCTGGC 18
| | | | | | | | | | | | | | | | | | | | | |
DB 4 CAGGAAGGACGCTGGC 20

RESULT 28
AAS08378
ID AAS08378 standard; DNA; 50 BP.
XX
XX AAS08378;
AC
DT 23-OCT-2001 (first entry)
XX
XX Pig PHGPX 3' UTR oligonucleotide #4.
XX
XX P1g; phospholipid hydroperoxide glutathione peroxidase; PHGPX;
KW Citrus stress-associated protein; Cit-SAP; antioxidant cosmetic;
KW peroxidation; skin ageing; necrosis; skin lightening supporting agent;
KW oligonucleotide; ss.
XX
XX Sus scrofa.
OS
XX
XX EP1111055-A1.
PN
PD 27-JUN-2001.
XX
XX 08-DEC-1999; 99EP-0403079.
PF
XX
XX 08-DEC-1999; 99EP-0403079.
PR
XX
XX (VETI-) VETIGEN.
PA
XX
XX Strosberg AD, Eshdat Y;
PI
XX
XX MPI; 2001-41936/45.
DR
XX
XX New phospholipid hydroperoxide glutathione peroxidase, useful for
PT manufacturing antioxidant cosmetic for preventing lipid and
PT phospholipid modification due to peroxidation, leading to damage of
PT skin cells, ageing or necrosis -
XX
XX
XX Example 6; Page 38; 61pp; English.
XX
XX The sequence represents an oligonucleotide used to construct the 3'

UTR of pig PHGPx. The pig 3' UTR is added to a cDNA encoding orange phospholipid hydroperoxide glutathione peroxidase (PHGPx) (Citrus stress-associated protein, Cit-SAP) mutein, for expression in eukaryotic cells. The mutein has the cysteine at position 41 in the wild-type mutated to a selenocysteine, in order that the activity of the plant enzyme will be increased to resemble that of animal PHGPx enzymes. The plant PHGPx, its analogues, and plant enzymes having PHGPx activity are useful for manufacturing an antioxidant cosmetic or pharmaceutical dermatological composition for preventing lipid and phospholipid modification due to their peroxidation, which may lead to damage of skin cells, ageing and/or necrosis. These may also be used to protect phospholipids used in cosmetic compositions against phospholipid oxidation, and as skin-lightening supporting agents.

Sequence 50 BP; 11 A; 10 C; 12 G; 17 T; 0 other;

Query Match	67.8%	Score 12.2	DB 22	Length 50:
Best Local Similarity	82.4%	Pred. No. 9.6e+03		
Matches 14:	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;

QY 1 CCCGGAGGCAGTCTGG 17
 . ||| ||||| ||||
Db 30 CCCACAGCAGCACTCG 46

RESULT 29
ABA97719/c
ID ABA97719 standard; DNA: 22 BP.
XX
XX ABA97719;
DT 18-JUN-2002 (first entry)
DE Wolfram Syndrome 1 gene vector screening primer.
XX
XX Wolfram Syndrome 1; WFS1; transgenic; wolfram; brain; depression;
KW stress-induced neurochemical change; behavioural change; mouse;
RW drug screening; antidepressant; primer; ss.
XX
OS unidentified.
XX
PN WO200191548-A2.
XX
PD 06-DEC-2001.
XX
PE 31-MAY-2001; 2001WO-US17652.
XX
PR 01-JUN-2000; 2000US-209394P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
PI Roberds SL, Huff RW;
DR WPI: 2002-089969/12.
XX
PT New transgenic non-human animals (mice), useful as models for
PT depression, for monitoring the efficacy of a drug against depression,
PT and for screening antidepressants, drugs or genes for ameliorating or
PT treating depression -
XX
PS Example 1; Page 47; 65pp; English.
CC
CC The present sequence represents a screening primer, designated MMF-SCI,
CC used to screen for homologous recombinants based on the Wolfram Syndrome
CC 1 (WFS1) gene vector sequence of the invention. The specification
CC describes a non-human transgenic mammal comprising a genome containing a
CC single copy of a wild-type WFS1 gene (see ABA97708) and a modified WFS1
CC allele containing a mutation that disrupts the function of wolframin, or
CC its transgenic progeny. Wolframin is a predicted transmembrane protein
CC expressed in many tissues including pancreas and brain. The transgenic
CC nonhuman animals are useful as models for depression, particularly as
CC models for depression in humans. The animals exhibit chronic
CC stress-induced neurochemical and behavioural changes associated with

CC depression. The transgenic animals are also useful for screening or
CC identifying antidepressant agents, drugs or genes that may be employed to
CC alleviate or treat depression. The animals are also useful for
CC monitoring the efficacy of a drug against depression.

XX Sequence 22 BP; 3 A; 8 C; 6 G; 5 T; 0 other;

Query Match 66.7%; Score 12; DB 24; Length 22;

Best Local Similarity 100.0%; Pred. No. 1.2e+04; Mismatches 0; Indels 0; Gaps 0;

QY 6 AAGCAGCTCTGG 17
DB 21 AAGCAGCTCTGG 10

RESULT 30
AAV41645/C
ID AAV41645 standard; DNA; 23 BP.

XX AAV41645;

XX 12-OCT-1998 (first entry)

XX Nucleotide sequence of PCR primer Neo-134R.

XX PCR; primer: amplification; transgenic animal; H2-M gene; cancer;
XX inflammatory disease; graft rejection; autoimmune disease; ss.

XX Synthetic.
XX Mus sp.

XX BP853122-A2.

XX 15-JUL-1998.

XX 09-JAN-1998; 98BP-0300149.

XX 10-JAN-1997; 97US-0780949.

XX (ORTH) ORTHO PHARM CORP.

XX Karlsson L, Leung W, Peterson PA, Zhou L;

XX WPI; 1998-364648/32.

XX New transgenic animals which lack functional H2-M gene - used to
XX develop agents for treating e.g. inflammation, graft rejection,
XX autoimmune disease or cancer

XX Example 3; Page 8; 21pp; English.

CC This is the nucleotide sequence of a PCR primer used for amplification
CC in the method of the invention involving novel transgenic animals
CC lacking functional the H2-M gene. The transgenic animals can be used
CC to establish a non-human model for diseases involving H2-M equivalents
CC such as HLA-DM in humans. They can be used to identify agents for use
CC in the treatment of e.g. inflammatory disease, graft rejection,
CC autoimmune diseases or cancer.

XX Sequence 23 BP; 5 A; 8 C; 5 G; 5 T; 0 other;

Query Match 66.7%; Score 12; DB 19; Length 23;

Best Local Similarity 100.0%; Pred. No. 1.2e+04; Mismatches 0; Indels 0; Gaps 0;

QY 6 AAGCAGCTCTGG 17
DB 23 AAGCAGCTCTGG 12

RESULT 31
ABQ03907/C

ID ABQ03907 standard; DNA; 24 BP.

XX ABQ03907;

XX 11-JUN-2002 (first entry)

XX Oligonucleotide adapter/capture probe 3898.

XX Oligonucleotide array; adapter sequence; probe; ss.

XX Synthetic.

XX WO200216649-A2.

XX 28-FEB-2002.

XX 27-AUG-2001; 2001WO-US26519.

XX 25-AUG-2000; 2000US-227948P.

XX 29-AUG-2000; 2000US-228854P.

XX (ILLU-) ILLUMINA INC.

XX Gundersen K;

XX WPI; 2002-292068/33.

XX Array comprising adapter sequences useful for immobilizing or detecting
XX a target nucleic acid sequence, has different addresses comprising
XX different specific capture probes

XX Claim 1; Page 136; 261pp; English.

XX The invention relates to an oligonucleotide array (1) comprising at least
XX 25 different addresses (adapter sequences) with each comprising a
XX different capture probe selected from a group consisting of the sequences
XX given in ABQ00010-ABQ13409. (1) is useful for immobilising a target
XX nucleic acid sequence by attaching a adapter nucleic acid
XX (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target
XX nucleic acid and contacting the modified target nucleic acid with (1).
XX The steps of above method is useful for detecting a target nucleic acid,
XX which further comprises detecting the presence of the modified target
XX nucleic acid.

XX Sequence 24 BP; 5 A; 7 C; 5 G; 7 T; 0 other;

Query Match 66.7%; Score 12; DB 24; Length 24;

Best Local Similarity 100.0%; Pred. No. 1.2e+04; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGGAGGCGAGTC 14
DB 19 CGGAGGCGAGTC 8

RESULT 32

AAAX00963/C

ID AAX00963 standard; DNA; 26 BP.

XX AAX00963;

XX 25-MAR-1999 (first entry)

XX ADA knock-out specific primer pkr.

XX Adenosine; neuronal activity; pain syndrome; epilepsy; immortalised;
XX ADA gene; acute trauma; osteoarthritis; burn; rheumatoid arthritis;

XX knock-out; PCR primer; ss.

XX Synthetic.
XX Mus sp.
XX WO9858653-A1.

PD	XX	30-DEC-1998.
FD	XX	
PE	XX	23-JUN-1996; 98WO-IB00973.
PR	XX	23-JUN-1997; 97US-0881038.
PA	XX	(BOIS/) BOISON D.
PA	XX	(MOHL/) MOHLER H.
PL	XX	Boison D, Mohler H;
DR	XX	WPI: 1999-081040/07.
PT	XX	Use of adenosine to inhibit neuronal activity in patient - by
PT	XX	delivering chronic local dose to a site of activity to inhibit pain
PT	XX	syndrome or epilepsy
PS	XX	Examples; Page 22; 43pp; English.
CC	XX	The invention relates to the use of adenosine for inhibiting neuronal
CC	XX	activity in a patient having pain syndrome or epilepsy. A chronic local
CC	XX	dose of adenosine delivered to a site of neuronal activity, inhibits the
CC	XX	neuronal activity at the site and inhibits the pain syndrome or
CC	XX	epilepsy. Methods of generating a conditionally immortalised
CC	XX	adenosine-releasing cells are also provided. One method comprises
CC	XX	generating a non-human animal embryo having an ADA gene (-/-) tsA58 (+/-)
CC	XX	genotype and isolating conditionally immortalised adenosine-releasing
CC	XX	cells from the embryo. The products and methods can be used for treating
CC	XX	epilepsy or pain syndromes, e.g. pain associated with soft tissue disease
CC	XX	and peripheral damage (e.g. acute trauma, osteoarthritis, rheumatoid
CC	XX	arthritis, burns, epistomy), spinal pain, musculo-skeletal pain,
CC	XX	upper extremity pain, myofascial pain syndromes, headache, deep and
CC	XX	visceral pain syndromes, (e.g. heart pain, muscle pain, eye pain,
CC	XX	orofacial pain, abdominal pain, gynecological pain and pain during
CC	XX	labour), pain associated with nerve and root damage (e.g. peripheral
CC	XX	nerve disorders or infections, amputation-induced pain, peripheral
CC	XX	neuropathies, tic douloureux and atypical facial pain, arachnoiditis),
CC	XX	carcinoma-induced pain (particularly that involving bone and soft tissue
CC	XX	carcinoma and metastases), and central nervous system-induced pain (such
CC	XX	as central pain due to spinal cord or brain stem damage). The local
CC	XX	delivery of adenosine exhibits therapeutic effects without involving side
CC	XX	effects associated with systemic administration. Sequences AXX00963-67
CC	XX	represent allele-specific PCR primers used for genotyping cell lines
CC	XX	having ADA gene (-/-) tsA58 (+/-) genotype. The present sequence is a ADA
CC	XX	knock-out specific primer specific for the PKA promoter of the neomycin
CC	XX	gene cassette used for the knock-out allele.
SQ	XX	Sequence 26 BP; 7 A; 7 C; 7 G; 5 T; 0 other;
Query Match		66.7%; Score 12; DB 20; Length 26;
Best Local Similarity		100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative		0; Mismatches 0; Indels 0; Gaps 0
Y	6	AAGCAGCTCTGG 17
Db	17	AAGCAGCTGG 6
RESULT 33		
AA501072/c		
ID	AA501072	standard; DNA; 26 BP.
XX	AA501072;	
XX	AC	
XX	DT	29-MAY-2001 (first entry)
XX	XX	PTKLR-Vn/VEGF 5' transgene PCR primer R51.
XX	XX	
XX	XX	Mouse: phosphoglycerate kinase 1 promoter; targeting construct;
KW	XX	transgenic animal; reporter expression cassette; luciferase;
KW	XX	vitronectin; FOS; galactin 3; VEGF; VEGFR; Tie2; selectable marker;
KW	XX	neomycin phosphotransferase II; chloramphenicol acetyltransferase;

KW	thymidine kinase; PCR primer; ss.
XX	
OS	Mus sp.
XX	
PN	WO200118225-A1.
XX	
PD	15-MAR-2001.
XX	
PE	16-DEC-1999; 99WO-US30078.
XX	
PR	03-SEP-1999; 99US-0152522.
XX	
PA	(XENO-) XENGEN CORP.
XX	
PI	Zhang N;
XX	
DR	WPI: 2001-203085/20.
PT	Targeting constructs and methods of using them for creating transgenic animals -
XX	
PS	Example 4; Page 53; 96pp; English.
CC	
CC	The present sequence for PCR primer F51 (AAS01071) to amplify a 1799 bp DNA fragment from the 5' end of the transgene that is integrated into the vitronectin site through homologous DNA recombination. The pTKR-Vn/VEGF targeting vector is an example of novel targeting constructs and methods of using them for creating transgenic animals in which at least 1 single-copy, non-essential gene is replaced with a reporter expression cassette (e.g. a luciferase gene linked to a promoter heterologous to the single-copy, non-essential gene). The single-copy, non-essential gene may be selected from vitronectin (Vn), fibroblast growth factor 3. The promoter element may be selected from VEGF, VEGFR and Tie2. The constructs may contain a selectable marker e.g. neomycin phosphotransferase II, chloramphenicol acetyltransferase and thymidine kinase. The constructs are useful for creating transgenic animals in which at least 1 single-copy, non-essential gene is replaced with a reporter expression cassette. Methods of using these animals are also described.
CC	
CC	
SQ	Sequence 26 BP; 6 A; 9 C; 7 G; 4 T; 0 other;
OY	Query Match 66.7%; Score 12; DB 22; Length 26; Best Local Similarity 100.0%; Pred. No. 1.2e+04; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
DG	6 AAGCAGCTGTGG 17 12 AAGCAGCTGTGG 1
RESULT 34	
AAF32217/C	
ID	AAF32217 standard; DNA; 26 BP.
AC	AAF32217;
DT	12-APR-2001 (first entry)
DE	Mouse Musashi 1 PCR primer SEQ ID NO:4.
KW	Mouse; Musashi 1; mutant; hydrocephaly; ontogenesis; PCR primer; ss.
OS	Mus sp.
PN	WO200101767-A1.
PD	11-JAN-2001.
EF	04-JUL-2000; 2000WO-JP04449.
PR	05-JUL-1999; 99JP-0190796.

PA	(NISC) JAPAN SCI & TECHNOLOGY CORP.
XX	
PI	Sakakibara S, Noda T, Okano H;
XX	
DR	WPI: 2001-138031/14.
XX	
PT	Hydrocephaly model animals obtained through ontogenesis of totipotent
PT	cell carrying a functionally deficient Musashi 1 gene, are useful in
XX	diagnosis and development of drugs for hydrocephaly
XX	
PS	Example; Page 16; 19pp; Japanese.
XX	
CC	The present invention describes hydrocephaly model animals which are
CC	not human mammals obtained through ontogenesis of a totipotent cell
CC	carrying a functionally deficient Musashi 1 gene transferred into them
CC	and their offspring, which are characterised by having the Musashi 1
CC	mutation gene in somatic chromosomes. The model animals are useful in
CC	studying the cause, diagnosis and development of drugs for congenital
CC	and difficult-to-treat hydrocephaly. With such animals, specific drugs
CC	and surgical procedures for hydrocephaly treatment can be obtained.
CC	AA63214 to AA63217 represent PCR primers for Musashi 1 which are
XX	used in an example from the present invention.
XX	
SQ	Sequence 26 BP; 6 A; 8 C; 7 G; 5 T; 0 other;
Query Match	66.7%; Score 12; DB 22; Length 26;
Best Local Similarity	100.0%; Pred. NO. 1.2e+04;
Matches 12; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	6 AAGCGAGTCTGG 17
DB	13 AAGCGAGTCTGG 2
RESULT 35	
AA662210/C	
ID	AA662210 standard; DNA; 28 BP.
XX	
AC	AA662210;
XX	
DT	21-MAY-2001 (first entry)
XX	
DE	PCR primer for PKG.
XX	
KW	Alpha-tocopherol transport protein; alpha-TTP; knockout animal; diabetes;
KW	alpha-TTP inhibitor; vitamin E deficiency; arteriosclerosis; mouse;
KW	oxidative stress; PCR primer; PKG; ss.
OS	Synthetic.
XX	
PN	WO200113716-A1.
XX	
PD	01-MAR-2001.
XX	
PF	24-AUG-2000; 2000WO-jP05686.
XX	
PR	24-AUG-1999; 99JP-0237003.
XX	
PA	(INOUE) INOUE K.
PA	(ARAI) ARAI H.
XX	
PI	Inoue K, Arai H, Arita M, Ushige K, Suzuki H;
XX	
DR	WPI: 2001-218381/22.
XX	
PT	alpha-tocopherol transport protein knock-out animal, useful as tool for
PT	clarifying onset mechanism of diseases based on oxidation stress e.g.
PT	import vitamin E deficiency, arteriosclerosis and diabetes, and in drug
XX	development
XX	
XX	Example 2; Page 10; 41pp; Japanese.
CC	This invention relates to an alpha-tocopherol transport protein

```

CC (alpha-TRP) knockout animal. The non-human mammal is useful as a tool for
CC determining the onset mechanisms of diseases which are based on
CC oxidation stress, e.g. inborn vitamin E deficiency, arteriosclerosis and
CC clabates. The present sequence represents a PCR primer specific for PKG.
CC
XX
SQ Sequence 28 BP; 6 A; 9 C; 7 G; 6 T; 0 other;

Query Match 66.7%; Score 12; DB 22; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 6 AGGCAGTCTGG 17
Db 27 AAGCAGTCTGG 16

RESULT 36
ABT03702/C
ID ABT03702 standard; DNA; 28 BP.
XX
AC ABT03702;
XX
DT 13-SEP-2002 (first entry)
DE
XX Human Neurogenin-3 gene PCR primer SEQ ID NO: 223.
XX
KW Human; cancer; neoplastic disease; tumour specific marker; cytostatic;
XX transcription factor; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200240716-A2.
XX
PD 23-MAY-2002.
XX
PF 13-NOV-2001; 2001WO-US43461.
XX
PR 16-NOV-2000; 2000US-249508P.
XX
PA (CEMT-1) CEMINES LLC.
XX
PI Palm K;
XX
DR WPI; 2002-537346/57.
XX
PR Determining the presence of neoplastic molecular markers, by
XX identifying the presence of markers in host test sample using array of
XX neoplastic molecular marker specific reagents and analyzing the array
XX of the reagents -
XX
XX Example 1; Page 17; 41pp; English.
XX
CC The present invention relates to a method for determining the presence of
CC neoplastic molecular markers in a host, involving the use of neoplastic
CC molecular marker specific reagents to detect such markers and analyzing
CC the array of reagents, allowing the identification of the neoplastic
CC disease present. This can be used to determine the best treatment for
CC cancers, in particular neural cell lung and prostate tumours. The
CC present sequence is a PCR primer useful for detecting the coding
CC sequences of markers of the invention.
CC
SQ Sequence 28 BP; 11 A; 7 C; 6 G; 4 T; 0 other;

Query Match 66.7%; Score 12; DB 24; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AGGCAGTCTGCC 18
Db 28 AGGCAGTCTGCC 17

RESULT 37

```

AAZ65981/c
ID AAZ65981 standard; DNA: 47 BP.
AC AAZ65981;
XX
XX
11-SEP-2001 (first entry)
XX
XX Human map-related diallelic marker SEQ ID NO:328.
DE
XX Human genome; diallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotypic; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW diagnosis; single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
FH Key location/Qualifiers
FT replace(24,G)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
XX W0954500-A2.
XX
XX 28-OCT-1999.
XX
XX 21-APR-1999; 99WO-IB00822.
XX
XX 21-APR-1998; 98US-0082614.
XX 23-NOV-1998; 98US-0109732.
XX
XX (GEST) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
XX
XX WPI: 2000-013267/01.
XX
XX Novel diallelic markers used to construct a high density disequilibrium
PT map of the human genome -
XX
XX Claim 1; Page 300; 2745pp; English.
XX
XX AAZ65654 to AAZ65578 represent human diallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ65579 to AAZ77440 represent amplification
CC primers for the diallelic markers. The diallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.
XX
XX
SQ Sequence 47 BP; 10 A; 15 C; 13 G; 9 T; 0 other;

Query Match 66.7%; Score 12; DB 21; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 AGGCGACTGCGC 18
DB 30 AGGCGACTGCGC 19

RESULT 38
AAZ76214/c
ID AAZ76214 standard; DNA: 15 BP.
XX

AC AAZ76214;
XX
XX 12-SEP-1997 (first entry)
XX
XX
XX Human IL4 receptor antisense oligonucleotide.
XX
XX Asthma; airway epithelium; adenosine free; cystic fibrosis;
KW chronic obstructive pulmonary disease; bronchitis; interleukin; ss.
XX
XX Synthetic.
XX
XX W09640162-A1.
XX
XX 19-DEC-1996.
XX
XX 06-JUN-1996; 96WO-US09306.
XX
XX 07-JUN-1995; 95US-0474497.
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX
XX Metzger WJ, Nyce JW;
XX
XX WPI: 1997-051871/05.
XX
XX Treatment of airway diseases such as asthma - by topically applying
PT adenosine-free antisense oligo:nucleotide to airway epithelium of
PT subject
XX
XX Example 5; Page 30; 71pp; English.
XX
XX A method for treating airway disease in a subject has been produced,
CC which involves the topical administration of an essentially adenosine
CC free antisense oligonucleotide (ON) to the airway epithelium of the
CC subject. The present sequence is an antisense oligonucleotide
CC specific for the human IL4 receptor. The method can be used to
CC treat airway diseases such as cystic fibrosis, asthma, chronic
CC obstructive pulmonary disease, bronchitis and other airway diseases
CC characterised by an inflammatory response. By eliminating adenosine from
CC the antisense ON, its liberation upon antisense degradation is
CC prevented, thereby preventing adenosine-induced bronchoconstriction in
CC patients with hyper-reactive airways.
XX
XX
SQ Sequence 15 BP; 0 A; 7 C; 4 G; 4 T; 0 other;

Query Match 65.6%; Score 11.8; DB 18; Length 15;
Best Local Similarity 86.7%; Pred. No. 1.4e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 GGAAGCGACTGCGC 18
DB 15 GGAAGCGAGCCAGCGC 1

RESULT 39
AAZ54009/c
ID AAZ54009 standard; DNA: 15 BP.
XX
XX AAZ54009;
XX
XX 05-JUL-1999 (first entry)
XX
XX Human IL-4 receptor antisense oligonucleotide fragment.
XX
XX Antisense oligonucleotide; multiple target; antisense treatment;
KW impaired respiration; inflammation; lung disease;
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;

KW prostate cancer; ss.
XX Synthetic.
OS WO9913886-A1.
PN 25-MAR-1999.
XX
XX 17-SEP-1998; 98WO-US19419.
XX
XX 09-JUN-1998; 98US-0093972.
PR 17-SEP-1997; 97US-0059160.
XX
XX (UYEC-) UNIV EAST CAROLINA.
PA
XX NYCE JW:
PI
XX WPI; 1999-229400/19.
DR
XX New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT vasoconstriction
PS Disclosure; Page 49; 120pp; English.
XX
XX The specification describes antisense oligonucleotides (AAK52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene
CC initiation codons, genomic flanking regions, intron-exon borders, the
CC 5'-end, the 3'-end and the junction between coding and non-coding
CC regions and all segments of RNAs encoding proteins associated with one
CC or more diseases, conditions or mixtures. The antisense oligonucleotides
CC may be derived from sequences AAK5272-74. These multiple target
CC oligonucleotides (specifically AAK55180-771) can be used for the
CC antisense treatment of diseases and conditions. Typical diseases and
CC conditions are those associated with impaired respiration and
CC inflammation, including lung diseases, pulmonary vasoconstriction,
CC inflammation, allergic rhinitis, acute asthma, allergies, asthma, impaired
CC respiration, respiratory distress syndrome, pain, cystic fibrosis,
CC pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic
CC obstructive pulmonary disease (COPD), and cancers such as leukemias,
CC lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer,
CC pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma,
CC hepatic metastases, as well as all types of cancers which may metastasize
CC or have metastasized to the lungs, including breast and prostate cancer.
XX
XX Sequence 15 BP; 0 A; 7 C; 4 G; 4 T; 0 other:
SQ
Query Match 65.6%; Score 11.8; DB 20; Length 15;
Best Local Similarity 86.7%; Pred. No. 1.4e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 4 GGAAGCAGCTGCGC 18
DB 15 GGAAGCAGCAGCGC 1
RESULT 40
AAFI9575/C
ID AAF19575 standard; DNA; 15 BP.
XX
XX AAF19575:
AC
XX
XX 14-MAR-2001 (first entry)
DT
XX
XX Human IL4 receptor polynucleotide fragment #1142.
DE
XX
XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiallergic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;

KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
XX Homo sapiens.
OS WO200062736-A2.
PN 26-OCT-2000.
XX
XX 24-MAR-2000; 2000WO-US08020.
XX
XX 06-APR-1999; 99US-0127958.
XX
XX (UYEC-) UNIV EAST CAROLINA.
PA
XX (NYCE-) NYCE J W.
PI
XX NYCE JW:
PI
XX WPI; 2000-679539/66.
DR
XX Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
PS Claim 14; Page 208; 1592pp; English.
XX
XX The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (1) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'universal' or alternative base.
CC (1) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiallergic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (1) can be used to down-regulate the
CC expression and/or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine molecules and their receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543, represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention.
XX
XX Sequence 15 BP; 0 A; 7 C; 4 G; 4 T; 0 other:
SQ
Query Match 65.6%; Score 11.8; DB 21; Length 15;
Best Local Similarity 86.7%; Pred. No. 1.4e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 4 GGAAGCAGCTGCGC 18
DB 15 GGAAGCAGCAGCGC 1
Search completed: December 2, 2002, 12:49:01
Job time : 269 secs

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OM nucleic - nucleic search, using sw model

Run on: December 2, 2002, 12:43:38 / Search time 47 Seconds
(without alignments)
117.451 Million cell updates/sec

Title: US-09-848-868-35

Perfect score: 18

Sequence: 1 ccggaagcagctctgc 18

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 441362 segs, 153338381 residues 609818

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued_Patents_NA:*

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6: /cgn2_6/ptodata/1/lna/backfiles.seq:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	length	DB	ID	Description																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																</
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C 101	10.8	60.0	40	4	US-09-452-817-14	Sequence 14, Appl	C 174	10.6	58.9	41	1	US-08-409-442a-65
C 102	10.8	60.0	41	2	US-08-448-418-29	Sequence 29, Appl	C 175	10.6	58.9	41	2	US-08-469-609a-65
C 103	10.8	60.0	42	1	US-07-885-689a-9	Sequence 9, Appl	C 176	10.6	58.9	41	3	US-09-143-190-65
C 104	10.8	60.0	47	4	US-09-338-907-249	Sequence 249, App	C 177	10.6	58.9	41	4	US-09-102-344-65
C 105	10.8	60.0	47	4	US-09-338-907-326	Sequence 326, App	C 178	10.6	58.9	42	1	US-08-105-483-225
C 106	10.8	60.0	47	4	US-09-218-207-249	Sequence 249, App	C 179	10.6	58.9	42	1	US-08-709-209-225
C 107	10.8	60.0	47	4	US-09-218-207-326	Sequence 326, App	C 180	10.6	58.9	42	1	US-08-458-101-225
C 108	10.8	60.0	50	2	US-08-709-368-2	Sequence 2, Appl	C 181	10.6	58.9	42	2	US-08-486-969-37
C 109	10.6	58.9	18	4	US-08-363-240a-1086	Sequence 1086, Ap	C 182	10.6	58.9	42	2	US-08-486-969-41
C 110	10.6	58.9	18	4	US-09-156-828b-28	Sequence 28, Appl	C 183	10.6	58.9	42	2	US-08-504-949-96
C 111	10.6	58.9	19	4	US-08-063-167a-41	Sequence 29, Appl	C 184	10.6	58.9	42	2	US-08-050-478-96
C 112	10.6	58.9	20	1	US-08-063-167a-41	Sequence 41, Appl	C 185	10.6	58.9	42	2	US-09-414-117-96
C 113	10.6	58.9	20	1	US-08-007-997a-41	Sequence 41, Appl	C 186	10.6	58.9	42	4	US-09-678-437-96
C 114	10.6	58.9	20	2	US-08-440-740a-41	Sequence 41, Appl	C 187	10.6	58.9	43	3	US-08-832-985-43
C 115	10.6	58.9	20	2	US-08-344-155c-41	Sequence 41, Appl	C 188	10.6	58.9	43	3	US-09-410-903-24
C 116	10.6	58.9	20	2	US-09-048-804-2	Sequence 2, Appl	C 189	10.6	58.9	44	1	US-08-259-148a-28
C 117	10.6	58.9	20	3	US-08-574-396-40	Sequence 40, Appl	C 190	10.6	58.9	44	2	US-07-876-941a-44
C 118	10.6	58.9	20	3	US-08-982-845b-41	Sequence 41, Appl	C 191	10.6	58.9	45	1	US-08-086-428b-119
C 119	10.6	58.9	20	3	US-08-866-340-55	Sequence 55, Appl	C 192	10.6	58.9	45	2	US-08-468-570-119
C 120	10.6	58.9	20	3	US-08-991-525b-41	Sequence 41, Appl	C 193	10.6	58.9	45	2	US-08-290-665a-223a
C 121	10.6	58.9	20	3	US-09-085-759-41	Sequence 41, Appl	C 194	10.6	58.9	45	5	PCT-US95-10398-92
C 122	10.6	58.9	20	4	US-09-128-496-41	Sequence 41, Appl	C 195	10.6	58.9	47	1	US-08-482-882-92
C 123	10.6	58.9	20	4	US-09-103-875-61	Sequence 61, Appl	C 196	10.6	58.9	47	1	US-08-483-389-92
C 124	10.6	58.9	20	4	US-08-973-568-40	Sequence 40, Appl	C 197	10.6	58.9	47	2	US-08-487-1130-92
C 125	10.6	58.9	20	4	US-09-488-744a-63	Sequence 63, Appl	C 198	10.6	58.9	47	2	US-08-473-503-92
C 126	10.6	58.9	20	4	US-09-009-490a-41	Sequence 41, Appl	C 199	10.6	58.9	47	2	US-08-483-932-92
C 127	10.6	58.9	20	4	US-09-295-593-19	Sequence 19, Appl	C 200	10.6	58.9	47	2	US-08-720-420a-92
C 128	10.6	58.9	20	5	PCT-US93-08101-41	Sequence 41, Appl	C 201	10.6	58.9	47	3	US-08-714-017-92
C 129	10.6	58.9	21	1	US-08-137-701-8	Sequence 8, Appl	C 202	10.6	58.9	47	3	US-08-475-680-92
C 130	10.6	58.9	21	2	US-08-860-299-1	Sequence 1, Appl	C 203	10.6	58.9	47	4	US-09-641-638-870
C 131	10.6	58.9	21	4	US-09-287-623-1	Sequence 1, Appl	C 204	10.6	58.9	49	4	US-09-318-448-29
C 132	10.6	58.9	21	4	US-09-156-828b-22	Sequence 22, Appl	C 205	10.4	57.8	15	4	US-08-311-486c-171u
C 133	10.6	58.9	22	3	US-08-477-934-27	Sequence 27, Appl	C 206	10.4	57.8	15	2	US-08-292-620a-374f
C 134	10.6	58.9	22	4	US-07-986-776a-27	Sequence 27, Appl	C 207	10.4	57.8	15	3	US-09-071-845-374
C 135	10.6	58.9	23	3	US-08-463-903-36	Sequence 36, Appl	C 208	10.4	57.8	18	1	US-08-358-171-16
C 136	10.6	58.9	23	4	US-07-935-695-36	Sequence 36, Appl	C 209	10.4	57.8	18	1	US-08-358-171-16
C 137	10.6	58.9	24	1	US-08-241-372-7	Sequence 36, Appl	C 210	10.4	57.8	18	2	US-08-111-486c-108f
C 138	10.6	58.9	24	1	US-08-110-294a-1	Sequence 7, Appl	C 211	10.4	57.8	18	2	US-08-117-952-397
C 139	10.6	58.9	24	2	US-08-389-926-1	Sequence 1, Appl	C 212	10.4	57.8	19	3	US-09-090-947-16
C 140	10.6	58.9	24	5	PCT-US95-05420-7	Sequence 7, Appl	C 213	10.4	57.8	20	1	US-09-091-952a-185f
C 141	10.6	58.9	25	4	US-09-341-007b-8	Sequence 8, Appl	C 214	10.4	57.8	20	1	US-08-480-784-9
C 142	10.6	58.9	26	1	US-07-724-500b-8	Sequence 8, Appl	C 215	10.4	57.8	20	1	US-08-483-553-9
C 143	10.6	58.9	26	2	US-08-859-998-1016	Sequence 1016, Ap	C 216	10.4	57.8	20	1	US-08-483-554b-9
C 144	10.6	58.9	26	3	US-08-974-899-22	Sequence 22, Appl	C 217	10.4	57.8	20	1	US-08-488-011b-9
C 145	10.6	58.9	26	4	US-09-225-928-1016	Sequence 1016, Ap	C 218	10.4	57.8	20	2	US-08-117-952-617
C 146	10.6	58.9	28	6	546668-49	Patent No. 546668	C 219	10.4	57.8	20	3	US-09-344-001-41
C 147	10.6	58.9	30	1	US-07-989-160-2	Sequence 2, Appl	C 220	10.4	57.8	20	3	US-09-165-186-228
C 148	10.6	58.9	30	1	US-08-448-736-2	Sequence 2, Appl	C 221	10.4	57.8	20	4	US-08-850-727-9
C 149	10.6	58.9	30	1	US-08-452-779-2	Sequence 2, Appl	C 222	10.4	57.8	20	4	US-09-313-932-228
C 150	10.6	58.9	30	1	US-08-445-065-2	Sequence 2, Appl	C 223	10.4	57.8	20	4	US-09-313-932-380
C 151	10.6	58.9	30	3	US-08-980-160a-5	Sequence 5, Appl	C 224	10.4	57.8	20	4	US-09-657-481a-89
C 152	10.6	58.9	30	3	US-08-959-524-2	Sequence 2, Appl	C 225	10.4	57.8	20	4	US-09-593-711a-115f
C 153	10.6	58.9	33	2	US-08-595-043a-83	Sequence 83, Appl	C 226	10.4	57.8	20	5	PCT-US95-10202-9
C 154	10.6	58.9	33	3	US-08-889-841b-48	Sequence 48, Appl	C 227	10.4	57.8	20	5	PCT-US95-10203-9
C 155	10.6	58.9	34	1	US-08-435-350-35	Sequence 35, Appl	C 228	10.4	57.8	21	4	PCT-US95-10220-9
C 156	10.6	58.9	34	2	US-08-861-459-24	Sequence 24, Appl	C 229	10.4	57.8	21	5	US-08-853-980-22
C 157	10.6	58.9	37	1	US-08-428-370a-13	Sequence 13, Appl	C 230	10.4	57.8	21	4	US-08-943-731-496
C 158	10.6	58.9	37	2	US-08-600-764-13	Sequence 13, Appl	C 231	10.4	57.8	22	1	US-07-977-284a-30
C 159	10.6	58.9	38	2	US-08-124-981a-21	Sequence 21, Appl	C 232	10.4	57.8	22	2	US-08-256-426b-30
C 160	10.6	58.9	38	3	US-09-037-190-19	Sequence 19, Appl	C 233	10.4	57.8	23	1	US-08-211-202-31
C 161	10.6	58.9	38	3	US-09-037-192-19	Sequence 19, Appl	C 234	10.4	57.8	23	1	US-08-017-619-11
C 162	10.6	58.9	38	3	US-09-037-143-13	Sequence 13, Appl	C 235	10.4	57.8	23	2	US-08-350-670a-57
C 163	10.6	58.9	38	4	US-09-049-691-19	Sequence 19, Appl	C 236	10.4	57.8	23	3	US-07-850-770-11
C 164	10.6	58.9	38	4	US-08-260-174-19	Sequence 19, Appl	C 237	10.4	57.8	23	3	US-09-050-783-11
C 165	10.6	58.9	38	4	US-09-338-128a-19	Sequence 19, Appl	C 238	10.4	57.8	23	3	PCT-US93-0159b-11
C 166	10.6	58.9	38	4	US-09-332-346-19	Sequence 19, Appl	C 239	10.4	57.8	23	5	US-08-859-998-807
C 167	10.6	58.9	38	4	US-09-037-192-19	Sequence 19, Appl	C 240	10.4	57.8	24	4	US-09-225-928-807
C 168	10.6	58.9	38	5	PCT-US92-0825b-11	Sequence 11, Appl	C 241	10.4	57.8	25	4	US-09-078-199-19
C 169	10.6	58.9	40	1	US-07-612-673-16	Sequence 16, Appl	C 242	10.4	57.8	25	4	US-09-078-199-20
C 170	10.6	58.9	40	1	US-08-539-666-17	Sequence 17, Appl	C 243	10.4	57.8	25	4	US-09-369-971-19
C 171	10.6	58.9	41	1	US-07-931-473b-65	Sequence 65, Appl	C 244	10.4	57.8	25	4	US-09-369-971-20
C 172	10.6	58.9	41	1	US-07-712-131c-65	Sequence 65, Appl	C 245	10.4	57.8	26	1	US-08-363-240a-409f
C 173	10.6	58.9	41	1	US-08-412-110-65	Sequence 65, Appl	C 246	10.4	57.8	36	1	US-08-363-240a-936f

[illegible]

247	10.4	57.8	36	2	US-08-292-620A-1279	Sequence 1279, Ap	C 320	10.2	56.7	33	4	US-09-304-186-64	Sequence 64, Appl
248	10.4	57.8	36	3	US-08-856-074A-10	Sequence 10, Appl	C 321	10.2	56.7	34	1	US-07-998-973A-10	Sequence 10, Appl
249	10.4	57.8	36	3	US-09-071-845-1279	Sequence 1279, Ap	C 322	10.2	56.7	34	2	US-08-452-800A-10	Sequence 10, Appl
250	10.4	57.8	38	1	US-08-211-203-44	Sequence 44, Appl	C 323	10.2	56.7	34	3	US-08-858-003-15	Sequence 15, Appl
251	10.4	57.8	38	1	US-08-373-124A-1199	Sequence 1199, Ap	C 324	10.2	56.7	34	3	US-09-078-166-15	Sequence 15, Appl
252	10.4	57.8	38	1	US-08-373-124A-1199	Sequence 1219, Ap	C 325	10.2	56.7	34	3	US-08-997-467-15	Sequence 15, Appl
253	10.4	57.8	38	1	US-08-435-628-1199	Sequence 1199, Ap	C 326	10.2	56.7	34	5	PCT-US92-11353-10	Sequence 15, Appl
254	10.4	57.8	38	1	US-08-435-628-1219	Sequence 1219, Ap	C 327	10.2	56.7	36	3	US-08-991-426-9	Sequence 9, Appl
255	10.4	57.8	38	2	US-08-293-620A-2039	Sequence 2039, Ap	C 328	10.2	56.7	36	3	US-08-968-563-16	Sequence 16, Appl
256	10.4	57.8	38	3	US-09-071-845-2039	Sequence 2039, Ap	C 329	10.2	56.7	36	3	US-08-968-563-16	Sequence 16, Appl
257	10.4	57.8	40	2	US-08-767-979-2039	Sequence 9, Appl	C 330	10.2	56.7	36	3	US-09-143-470-8	Sequence 8, Appl
258	10.4	57.8	40	2	US-09-295-026-9	Sequence 9, Appl	C 331	10.2	56.7	36	3	US-09-143-470-8	Sequence 8, Appl
259	10.4	57.8	50	2	US-08-389-564B-29	Sequence 29, Appl	C 332	10.2	56.7	36	3	US-08-968-563A-26	Sequence 26, Appl
260	10.4	57.8	50	3	US-08-389-564B-30	Sequence 30, Appl	C 333	10.2	56.7	36	3	US-08-968-563A-26	Sequence 26, Appl
261	10.4	57.8	50	3	US-08-466-047B-29	Sequence 29, Appl	C 334	10.2	56.7	36	3	US-09-311-872A-14	Sequence 14, Appl
262	10.4	57.8	50	3	US-08-466-047B-30	Sequence 30, Appl	C 335	10.2	56.7	36	4	US-09-307-872A-14	Sequence 14, Appl
263	10.4	57.8	50	3	US-08-983-607B-30	Sequence 30, Appl	C 336	10.2	56.7	36	4	US-09-307-872A-14	Sequence 14, Appl
264	10.4	57.8	50	3	US-08-983-607B-30	Sequence 30, Appl	C 337	10.2	56.7	37	1	US-08-290-562E-15	Sequence 15, Appl
265	10.2	56.7	16	4	US-09-156-828B-23	Sequence 43, Appl	C 338	10.2	56.7	37	1	US-08-290-562E-15	Sequence 15, Appl
266	10.2	56.7	17	4	US-09-156-828B-23	Sequence 27, Appl	C 339	10.2	56.7	37	5	PCT-US95-10053-12	Sequence 12, Appl
267	10.2	56.7	17	4	US-08-584-940-7245	Sequence 27, Appl	C 340	10.2	56.7	40	4	US-09-476-281-23	Sequence 23, Appl
268	10.2	56.7	18	3	US-09-255-911-23	Sequence 23, Appl	C 341	10.2	56.7	41	4	US-08-962-281-23	Sequence 23, Appl
269	10.2	56.7	19	1	US-08-584-940-8297	Sequence 8297, Ap	C 342	10.2	56.7	44	1	US-07-885-889A-4	Sequence 4, Appl
270	10.2	56.7	19	1	US-08-604-773-1	Sequence 1, Appl	C 343	10.2	56.7	44	1	US-08-344-695-3	Sequence 3, Appl
271	10.2	56.7	20	1	US-08-309-167A-6	Sequence 64, Appl	C 344	10.2	56.7	45	1	US-08-288-405A-17	Sequence 17, Appl
272	10.2	56.7	20	1	US-08-063-167A-6	Sequence 64, Appl	C 345	10.2	56.7	45	1	US-08-605-785-782	Sequence 782, Ap
273	10.2	56.7	20	1	US-08-007-997A-64	Sequence 64, Appl	C 346	10.2	56.7	47	4	US-08-641-638-1286	Sequence 1286, Ap
274	10.2	56.7	20	1	US-08-389-067-15	Sequence 64, Appl	C 347	10.2	56.7	50	1	US-07-718-490-1	Sequence 1, Appl
275	10.2	56.7	20	2	US-08-440-740A-64	Sequence 64, Appl	C 348	10.2	56.7	50	1	US-08-765-176-3	Sequence 344, Ap
276	10.2	56.7	20	2	US-08-344-155C-64	Sequence 64, Appl	C 349	10.2	56.7	16	1	US-08-311-760A-344	Sequence 344, Ap
277	10.2	56.7	20	2	US-08-982-845B-64	Sequence 64, Appl	C 350	10.2	56.7	16	2	US-08-774-310-34	Sequence 344, Ap
278	10.2	56.7	20	3	US-08-982-845B-64	Sequence 64, Appl	C 351	10.2	56.7	19	2	US-09-357-072-31	Sequence 31, Appl
279	10.2	56.7	20	3	US-08-982-845B-64	Sequence 64, Appl	C 352	10.2	56.7	19	2	US-09-357-072-31	Sequence 31, Appl
280	10.2	56.7	20	3	US-09-085-759-64	Sequence 95, Appl	C 353	10.2	56.7	19	2	US-08-611-280-6	Sequence 344, Ap
281	10.2	56.7	20	4	US-09-288-461-95	Sequence 64, Appl	C 354	10.2	56.7	19	4	US-09-195-990-6	Sequence 6, Appl
282	10.2	56.7	20	4	US-08-974-549A-551	Sequence 551, Appl	C 355	10.2	56.7	20	1	US-09-562-466-6	Sequence 6, Appl
283	10.2	56.7	20	4	US-09-128-496-64	Sequence 64, Appl	C 356	10.2	56.7	20	2	US-07-872-678A-27	Sequence 27, Appl
284	10.2	56.7	20	4	US-09-161-540-14	Sequence 14, Appl	C 357	10.2	56.7	20	3	US-08-964-723-12	Sequence 12, Appl
285	10.2	56.7	20	4	US-09-487-445-35	Sequence 35, Appl	C 358	10.2	56.7	20	4	US-08-646-789A-17	Sequence 17, Appl
286	10.2	56.7	20	4	US-09-009-490A-64	Sequence 64, Appl	C 359	10.2	56.7	20	4	US-08-397-220B-60	Sequence 60, Appl
287	10.2	56.7	20	4	US-09-578-324-1	Sequence 1, Appl	C 360	10.2	56.7	20	4	US-08-650-093C-60	Sequence 60, Appl
288	10.2	56.7	20	4	US-09-167-109-205	Sequence 205, Appl	C 361	10.2	56.7	20	4	US-08-561-497-15	Sequence 15, Appl
289	10.2	56.7	20	5	PCT-US93-08101-64	Sequence 12, Appl	C 362	10.2	56.7	20	4	US-08-650-093C-60	Sequence 60, Appl
290	10.2	56.7	21	2	US-08-837-190C-20	Sequence 20, Appl	C 363	10.2	56.7	21	1	US-08-451-777A-8	Sequence 8, Appl
291	10.2	56.7	21	1	US-09-243-335-28	Sequence 28, Appl	C 364	10.2	56.7	21	1	US-08-451-777A-8	Sequence 8, Appl
292	10.2	56.7	22	1	US-08-344-960-9	Sequence 9, Appl	C 365	10.2	56.7	21	2	US-08-998-208-8	Sequence 8, Appl
293	10.2	56.7	23	3	US-08-755-587-163	Sequence 163, Appl	C 366	10.2	56.7	21	2	US-08-998-208-8	Sequence 8, Appl
294	10.2	56.7	24	4	US-09-034-088A-15	Sequence 15, Appl	C 367	10.2	56.7	23	4	US-09-225-928-655	Sequence 655, Appl
295	10.2	56.7	25	1	US-08-271-880A-137	Sequence 137, Appl	C 368	10.2	56.7	24	1	US-08-240-547-11	Sequence 11, Appl
296	10.2	56.7	25	1	US-08-315-671-3	Sequence 3, Appl	C 369	10.2	56.7	24	1	US-08-466-860-67	Sequence 67, Appl
297	10.2	56.7	25	2	US-08-858-933-3	Sequence 3, Appl	C 370	10.2	56.7	24	3	US-08-472-040A-67	Sequence 67, Appl
298	10.2	56.7	25	3	US-08-910-408-137	Sequence 137, Appl	C 371	10.2	56.7	24	3	US-08-513-974B-220	Sequence 220, Appl
299	10.2	56.7	25	3	US-09-344-920-4	Sequence 4, Appl	C 372	10.2	56.7	24	3	US-08-973-068-42	Sequence 42, Appl
300	10.2	56.7	25	4	US-09-168-406A-4	Sequence 4, Appl	C 373	10.2	56.7	24	4	US-08-276-776-67	Sequence 67, Appl
301	10.2	56.7	27	2	US-08-418-085-25	Sequence 25, Appl	C 374	10.2	56.7	24	4	US-08-471-309-67	Sequence 67, Appl
302	10.2	56.7	27	4	US-09-099-011A-25	Sequence 25, Appl	C 375	10.2	56.7	26	4	US-08-869-276-19	Sequence 19, Appl
303	10.2	56.7	27	4	US-09-243-335-20	Sequence 20, Appl	C 376	10.2	56.7	26	4	US-09-635-344-19	Sequence 19, Appl
304	10.2	56.7	28	3	US-08-743-637B-125	Sequence 125, Appl	C 377	10.2	56.7	26	4	US-09-398-629-19	Sequence 19, Appl
305	10.2	56.7	28	3	US-08-526-840B-125	Sequence 125, Appl	C 378	10.2	56.7	27	3	US-08-513-974B-114	Sequence 114, Appl
306	10.2	56.7	28	3	US-08-968-563-33	Sequence 33, Appl	C 379	10.2	56.7	28	1	US-08-954-470-8	Sequence 8, Appl
307	10.2	56.7	28	3	US-08-968-563-33	Sequence 39, Appl	C 380	10.2	56.7	28	2	US-09-129-852A-8	Sequence 8, Appl
308	10.2	56.7	29	1	US-08-166-664-1	Sequence 1, Appl	C 381	10.2	56.7	28	4	US-09-247-152A-8	Sequence 8, Appl
309	10.2	56.7	29	2	US-08-481-793-8	Sequence 8, Appl	C 382	10.2	56.7	28	4	US-09-257-793-8	Sequence 8, Appl
310	10.2	56.7	29	2	US-08-354-326-8	Sequence 8, Appl	C 383	10.2	56.7	29	3	US-08-320-912A-15	Sequence 15, Appl
311	10.2	56.7	29	5	PCT-US95-026E-8	Sequence 8, Appl	C 384	10.2	56.7	30	1	US-08-458-568A-7	Sequence 7, Appl
312	10.2	56.7	32	1	US-07-621-006B-8	Sequence 8, Appl	C 385	10.2	56.7	30	2	US-08-872-094-10	Sequence 10, Appl
313	10.2	56.7	32	1	US-08-018-489C-8	Sequence 8, Appl	C 386	10.2	56.7	30	3	US-08-687-421-102	Sequence 102, Appl
314	10.2	56.7	32	2	US-08-942-443-59	Sequence 59, Appl	C 387	10.2	56.7	33	2	US-08-577-492-29	Sequence 29, Appl
315	10.2	56.7	33	1	US-08-942-443-59	Sequence 64, Appl	C 388	10.2	56.7				
316	10.2	56.7	33	1	US-08-010-099-62	Sequence 62, Appl	C 389	10.2	56.7				
317	10.2	56.7	33	1	US-08-010-099-62	Sequence 64, Appl	C 390	10.2	56.7				
318	10.2	56.7	33	1	US-08-426-716-64	Sequence 64, Appl	C 391	10.2	56.7				
319	10.2	56.7	33	4	US-08-427-569-34	Sequence 34, Appl	C 392	10.2	56.7				

C 393	10	55.6	33	4	US-09-079-630-29	Sequence 29, Appl	466	9.8	54.4	20	3	US-09-289-267-61	Sequence 61, Appl
C 394	10	55.6	34	2	US-08-762-428A-8	Sequence 8, Appl	467	9.8	54.4	20	3	US-08-765-889C-6	Sequence 6, Appl
C 395	10	55.6	36	2	US-08-889-909A-17	Sequence 17, Appl	468	9.8	54.4	20	4	US-09-513-729B-68	Sequence 68, Appl
C 396	10	55.6	36	4	US-09-156-163A-17	Sequence 17, Appl	469	9.8	54.4	20	4	US-08-843-417-4	Sequence 4, Appl
C 397	10	55.6	39	2	US-08-750-810-5	Sequence 5, Appl	470	9.8	54.4	20	4	US-09-240-639-24	Sequence 24, Appl
C 398	10	55.6	39	2	US-08-244-548-2	Sequence 2, Appl	471	9.8	54.4	20	4	US-09-387-341-226	Sequence 226, App
C 399	10	55.6	40	1	US-08-199-507B-14	Sequence 14, Appl	472	9.8	54.4	20	4	US-09-851-896-19	Sequence 19, Appl
C 400	10	55.6	40	1	US-08-441-828-14	Sequence 14, Appl	473	9.8	54.4	20	4	US-09-658-679A-11	Sequence 11, Appl
C 401	10	55.6	40	2	US-08-470-939-42	Sequence 42, Appl	474	9.8	54.4	20	5	PCT-US95-07855-6	Sequence 6, Appl
C 402	10	55.6	40	4	US-09-113-750A-57	Sequence 57, Appl	475	9.8	54.4	21	2	US-08-753-979A-35	Sequence 35, Appl
C 403	10	55.6	40	4	US-09-141-027-14	Sequence 14, Appl	476	9.8	54.4	21	2	US-08-781-650B-4	Sequence 4, Appl
C 404	10	55.6	40	4	US-09-141-027-16	Sequence 16, Appl	477	9.8	54.4	21	4	US-09-493-461-10	Sequence 10, Appl
C 405	10	55.6	40	4	US-09-141-027-18	Sequence 18, Appl	478	9.8	54.4	21	4	US-09-493-461-18	Sequence 18, Appl
C 406	10	55.6	40	5	PCT-US96-09452-42	Sequence 42, Appl	479	9.8	54.4	21	4	US-09-177-650-13	Sequence 13, Appl
C 407	10	55.6	41	4	US-09-564-805-182	Sequence 182, Appl	480	9.8	54.4	22	1	US-08-479-723A-87	Sequence 87, Appl
C 408	10	55.6	42	3	US-08-955-636-12	Sequence 12, Appl	481	9.8	54.4	22	4	US-09-068-860-2	Sequence 2, Appl
C 409	10	55.6	42	4	US-09-202-101-13	Sequence 13, Appl	482	9.8	54.4	22	4	US-09-068-860-41	Sequence 41, Appl
C 410	10	55.6	42	4	US-09-191-468-18	Sequence 18, Appl	483	9.8	54.4	22	4	US-09-068-805-6	Sequence 6, Appl
C 411	10	55.6	43	1	US-08-253-877C-34	Sequence 34, Appl	484	9.8	54.4	22	4	US-09-068-805-7	Sequence 7, Appl
C 412	10	55.6	43	2	US-08-452-164A-34	Sequence 34, Appl	485	9.8	54.4	22	4	US-09-068-805-11	Sequence 11, Appl
C 413	10	55.6	45	2	US-08-690-495-23	Sequence 23, Appl	486	9.8	54.4	23	1	US-08-479-723A-78	Sequence 78, Appl
C 414	10	55.6	45	2	US-08-690-494-23	Sequence 23, Appl	487	9.8	54.4	23	2	US-08-823-516-105	Sequence 105, App
C 415	10	55.6	45	5	PCT-US95-07671-23	Sequence 23, Appl	488	9.8	54.4	23	3	US-08-759-038-90	Sequence 90, Appl
C 416	10	55.6	48	1	US-08-105-483-95	Sequence 95, Appl	489	9.8	54.4	23	3	US-08-758-314-90	Sequence 90, Appl
C 417	10	55.6	48	1	US-08-196-538-5	Sequence 5, Appl	490	9.8	54.4	23	4	US-09-092-077-48	Sequence 48, Appl
C 418	10	55.6	48	1	US-08-709-209-95	Sequence 95, Appl	491	9.8	54.4	23	4	US-09-068-805-8	Sequence 8, Appl
C 419	10	55.6	48	1	US-08-458-101-95	Sequence 95, Appl	492	9.8	54.4	24	2	US-08-859-998-864	Sequence 964, App
C 420	10	55.6	48	2	US-08-558-269-20	Sequence 20, Appl	493	9.8	54.4	24	3	US-08-483-316-2	Sequence 2, Appl
C 421	10	55.6	48	4	US-09-410-882-20	Sequence 20, Appl	494	9.8	54.4	24	4	US-09-074-658-74	Sequence 74, Appl
C 422	10	55.6	50	1	US-08-384-708A-117	Sequence 117, App	495	9.8	54.4	24	4	US-08-506-286B-15	Sequence 15, Appl
C 423	10	55.6	50	4	US-08-687-421-117	Sequence 117, App	496	9.8	54.4	24	4	US-09-225-928-864	Sequence 964, App
C 424	10	55.6	50	4	US-07-936-463-6	Sequence 6, Appl	497	9.8	54.4	24	5	PCT-US95-12624-2	Sequence 2, Appl
C 425	10	55.6	50	4	US-08-472-240A-26	Sequence 26, Appl	498	9.8	54.4	25	4	US-09-315-734-30	Sequence 30, Appl
C 426	9.8	54.4	17	4	US-08-584-040-2349	Sequence 2349, Ap	499	9.8	54.4	25	4	US-09-389-341-10	Sequence 30, Appl
C 427	9.8	54.4	17	4	US-08-584-040-5803	Sequence 5803, Ap	500	9.8	54.4	25	4	US-09-318-562A-77	Sequence 15, Appl
C 428	9.8	54.4	17	4	US-08-584-040-6031	Sequence 6031, Ap	501	9.8	54.4	26	2	US-09-318-503-18	Sequence 18, Appl
C 429	9.8	54.4	18	1	US-07-685-722A-2	Sequence 2, Appl	502	9.8	54.4	26	4	US-09-293-170-35	Sequence 35, Appl
C 430	9.8	54.4	18	1	US-08-053-867A-9	Sequence 9, Appl	503	9.8	54.4	26	4	US-08-758-306-310	Sequence 310, App
C 431	9.8	54.4	18	1	US-08-050-073-278	Sequence 278, App	504	9.8	54.4	27	1	US-08-758-306-694	Sequence 894, App
C 432	9.8	54.4	18	2	US-08-585-684B-2552	Sequence 2552, Ap	505	9.8	54.4	27	1	US-08-758-306-1272	Sequence 1272, Ap
C 433	9.8	54.4	18	2	US-08-585-684B-2553	Sequence 16, Appl	506	9.8	54.4	27	1	US-08-506-296B-39	Sequence 39, Appl
C 434	9.8	54.4	18	3	US-09-106-038A-16	Sequence 17, Appl	507	9.8	54.4	27	4	US-08-584-040-6301	Sequence 6301, Ap
C 435	9.8	54.4	18	3	US-09-106-038A-17	Sequence 2, Appl	508	9.8	54.4	27	4	US-09-294-894-6	Sequence 6, Appl
C 436	9.8	54.4	18	3	US-09-255-911-2	Sequence 2, Appl	509	9.8	54.4	27	6	5387505-2	Patent No. 5387505
C 437	9.8	54.4	18	3	US-08-972-799A-18	Sequence 18, Appl	510	9.8	54.4	27	6	US-08-666-493-26	Sequence 26, Appl
C 438	9.8	54.4	18	3	US-09-195-666A-31	Sequence 31, Appl	511	9.8	54.4	28	2	US-08-859-998-546	Sequence 546, App
C 439	9.8	54.4	18	3	US-09-195-666A-32	Sequence 32, Appl	512	9.8	54.4	28	2	US-09-225-928-546	Sequence 546, App
C 440	9.8	54.4	18	4	US-09-038-073-2552	Sequence 2552, Ap	513	9.8	54.4	28	4	US-08-301-374-8	Sequence 8, Appl
C 441	9.8	54.4	18	4	US-09-038-073-2553	Sequence 2553, Ap	514	9.8	54.4	28	4	US-08-170-588-2	Sequence 2, Appl
C 442	9.8	54.4	18	4	US-09-506-282-18	Sequence 18, Appl	515	9.8	54.4	30	1	US-08-623-195-15	Sequence 15, Appl
C 443	9.8	54.4	18	4	US-09-632-380A-30	Sequence 30, Appl	516	9.8	54.4	30	1	US-08-184-1009-201	Sequence 201, App
C 444	9.8	54.4	18	4	US-09-630-706-32	Sequence 32, Appl	517	9.8	54.4	30	2	US-08-482-182-2	Sequence 2, Appl
C 445	9.8	54.4	18	4	US-08-584-040-6246	Sequence 6246, Ap	518	9.8	54.4	30	2	US-08-458-336-201	Sequence 201, App
C 446	9.8	54.4	18	4	US-09-635-705-31	Sequence 31, Appl	519	9.8	54.4	30	2	US-08-460-736-201	Sequence 201, App
C 447	9.8	54.4	18	4	US-09-635-705-32	Sequence 32, Appl	520	9.8	54.4	30	4	US-08-891-292A-64	Sequence 64, Appl
C 448	9.8	54.4	18	4	US-09-634-858A-31	Sequence 31, Appl	521	9.8	54.4	30	4	US-09-039-962A-49	Sequence 49, Appl
C 449	9.8	54.4	18	4	US-09-634-858A-32	Sequence 32, Appl	522	9.8	54.4	31	4	US-09-039-962A-49	Sequence 49, Appl
C 450	9.8	54.4	18	5	PCT-US95-03339-18	Sequence 18, Appl	523	9.8	54.4	31	4	US-08-679-645-269	Sequence 269, App
C 451	9.8	54.4	19	1	US-08-050-073-277	Sequence 277, App	524	9.8	54.4	31	4	US-09-194-285-41	Sequence 41, Appl
C 452	9.8	54.4	19	1	US-08-456-923-11	Sequence 11, Appl	525	9.8	54.4	31	4	US-09-042-482D-49	Sequence 49, Appl
C 453	9.8	54.4	19	1	US-08-376-362A-6	Sequence 6, Appl	526	9.8	54.4	31	4	US-08-913-612A-55	Sequence 55, Appl
C 454	9.8	54.4	19	2	US-08-690-734A-83	Sequence 83, Appl	527	9.8	54.4	31	4	US-08-835-728D-55	Sequence 55, Appl
C 455	9.8	54.4	19	3	US-08-742-185-83	Sequence 83, Appl	528	9.8	54.4	32	3	US-08-835-728D-55	Sequence 55, Appl
C 456	9.8	54.4	19	4	US-09-038-637-140	Sequence 140, App	529	9.8	54.4	32	3	US-08-835-728D-159	Sequence 159, App
C 457	9.8	54.4	19	4	US-08-478-316-93	Sequence 93, Appl	530	9.8	54.4	32	4	US-09-490-558-159	Sequence 159, App
C 458	9.8	54.4	19	4	US-08-874-569B-17	Sequence 17, Appl	531	9.8	54.4	32	4	US-08-891-292A-64	Sequence 64, Appl
C 459	9.8	54.4	19	4	US-09-457-708-19	Sequence 19, Appl	532	9.8	54.4	32	4	US-09-234-326-8	Sequence 8, Appl
C 460	9.8	54.4	19	4	US-09-019-793A-93	Sequence 93, Appl	533	9.8	54.4	32	4	US-08-438-639-57	Sequence 57, Appl
C 461	9.8	54.4	20	1	US-08-484-192-72	Sequence 72, Appl	534	9.8	54.4	33	1	US-07-813-338A-57	Sequence 57, Appl
C 462	9.8	54.4	20	1	US-08-484-192-129	Sequence 129, App	535	9.8	54.4	33	1	US-08-470-124-67	Sequence 67, Appl
C 463	9.8	54.4	20	2	US-08-651-692-6	Sequence 6, Appl	536	9.8	54.4	33	2	US-09-078-459-73	Sequence 73, Appl
C 464	9.8	54.4	20	3	US-08-940-250-19	Sequence 19, Appl	537	9.8	54.4	33	2	US-08-441-971-133	Sequence 133, App
C 465	9.8	54.4	20	3	US-09-011-821-4	Sequence 4, Appl	538	9.8	54.4	33	3		

539	9.8	54.4	33	4	US-08-321-653-133	Sequence 133, App	C 612	9.6	53.3	20	1	US-08-050-073-114	Sequence 114, App
540	9.8	54.4	33	4	US-08-442-144A-133	Sequence 133, App	C 613	9.6	53.3	20	1	US-08-321-990-38	Sequence 38, App
541	9.8	54.4	33	4	US-08-830-828A-133	Sequence 14, App	C 614	9.6	53.3	20	1	US-08-167-122-38	Sequence 38, App
542	9.8	54.4	33	4	US-08-441-920A-133	Sequence 133, App	C 615	9.6	53.3	20	1	US-08-157-952-50	Sequence 50, App
543	9.8	54.4	33	5	PCT-US94-10257A-94	Sequence 94, App	C 616	9.6	53.3	20	2	US-08-417-352-30	Sequence 30, App
544	9.8	54.4	34	4	US-09-167-98A-14	Sequence 14, App	C 617	9.6	53.3	20	2	US-08-688-352-30	Sequence 30, App
545	9.8	54.4	36	1	US-07-727-95A-11	Sequence 1, App	C 618	9.6	53.3	20	2	US-08-673-211-34	Sequence 34, App
546	9.8	54.4	36	1	US-07-834-53A-11	Sequence 11, App	C 619	9.6	53.3	20	3	US-08-649-816-2	Sequence 2, App
547	9.8	54.4	36	1	US-08-084-75B-1	Sequence 1, App	C 620	9.6	53.3	20	3	US-08-617-256-7	Sequence 7, App
548	9.8	54.4	36	1	US-08-436-53A-11	Sequence 11, App	C 621	9.6	53.3	20	3	US-08-286-904-6	Sequence 6, App
549	9.8	54.4	36	1	US-08-053-604-3	Sequence 3, App	C 622	9.6	53.3	20	4	US-09-287-141-7	Sequence 7, App
550	9.8	54.4	36	1	US-08-203-387-3	Sequence 3, App	C 623	9.6	53.3	20	4	US-09-433-613-7	Sequence 7, App
551	9.8	54.4	36	1	US-09-845-641-19	Sequence 19, App	C 624	9.6	53.3	20	4	US-09-504-245-7	Sequence 7, App
552	9.8	54.4	36	1	US-08-026-762-19	Sequence 19, App	C 625	9.6	53.3	20	4	US-09-287-662-7	Sequence 7, App
553	9.8	54.4	36	2	US-08-800-353-11	Sequence 11, App	C 626	9.6	53.3	20	4	US-09-287-679-7	Sequence 7, App
554	9.8	54.4	36	2	US-08-800-353-11	Sequence 11, App	C 627	9.6	53.3	20	4	US-09-397-766-7	Sequence 7, App
555	9.8	54.4	36	4	US-09-042-353-187	Sequence 187, App	C 628	9.6	53.3	20	4	US-09-287-681-7	Sequence 7, App
556	9.8	54.4	36	4	US-08-417A-35	Sequence 35, App	C 629	9.6	53.3	20	4	US-09-662-249A-32	Sequence 32, App
557	9.8	54.4	36	5	PCT-US92-06185-11	Sequence 11, App	C 630	9.6	53.3	20	4	US-09-495-444-7	Sequence 7, App
558	9.8	54.4	36	5	PCT-US92-06185-11	Sequence 11, App	C 631	9.6	53.3	20	4	US-09-337-388-2	Sequence 2, App
559	9.8	54.4	37	1	US-08-255-670A-7	Sequence 7, App	C 632	9.6	53.3	20	4	US-09-742-703-20	Sequence 20, App
560	9.8	54.4	38	1	US-08-390-850-838	Sequence 838, App	C 633	9.6	53.3	20	4	US-08-702-327-14	Sequence 14, App
561	9.8	54.4	38	1	US-08-373-124A-1694	Sequence 1694, App	C 634	9.6	53.3	20	4	US-08-943-731-360	Sequence 360, App
562	9.8	54.4	38	1	US-08-435-634-838	Sequence 838, App	C 635	9.6	53.3	20	4	US-08-643-181-28	Sequence 28, App
563	9.8	54.4	38	2	US-08-435-628-1694	Sequence 1694, App	C 636	9.6	53.3	20	4	US-08-955-138-58	Sequence 58, App
564	9.8	54.4	38	2	US-08-435-628-1694	Sequence 1694, App	C 637	9.6	53.3	20	4	US-08-859-998-1201	Sequence 1201, App
565	9.8	54.4	38	3	US-09-071-845-2271	Sequence 2271, App	C 638	9.6	53.3	20	4	US-09-661-764A-23	Sequence 23, App
566	9.8	54.4	39	1	US-08-053-131-60	Sequence 60, App	C 641	9.6	53.3	20	4	US-09-225-928-1201	Sequence 1201, App
567	9.8	54.4	39	1	US-08-645-641-60	Sequence 60, App	C 642	9.6	53.3	20	4	US-08-556-965-3	Sequence 3, App
568	9.8	54.4	39	1	US-08-096-762-60	Sequence 60, App	C 643	9.6	53.3	20	4	US-08-946-914-46	Sequence 46, App
569	9.8	54.4	39	2	US-08-800-353-48	Sequence 48, App	C 644	9.6	53.3	20	4	US-08-946-914-46	Sequence 46, App
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571	9.8	54.4	39	2	US-08-800-353-48	Sequence 48, App	C 646	9.6	53.3	20	4	US-08-946-914-46	Sequence 46, App
572	9.8	54.4	39	2	US-08-800-353-48	Sequence 48, App	C 647	9.6	53.3	20	4	US-08-946-914-46	Sequence 46, App
573	9.8	54.4	39	2	US-08-800-353-48	Sequence 48, App	C 648	9.6	53.3	20	4	US-08-946-914-46	Sequence 46, App
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575	9.8	54.4	39	2	US-08-800-353-48	Sequence 48, App	C 650	9.6	53.3	20	4	US-08-946-914-46	Sequence 46, App
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585	9.8	54.4	39	2	US-08-800-353-48	Sequence 48, App	C 660	9.6	53.3	20	4	US-08-946-914-46	Sequence 46, App
586	9.8	54.4	39	2	US-08-800-353-48	Sequence 48, App	C 661	9.6	53.3	20	4	US-08-946-914-46	Sequence 46, App
587	9.8	54.4	39	2	US-08-800-353-48	Sequence 48, App	C 662	9.6	53.3	20	4	US-08-946-914-46	Sequence 46, App
588	9.8	54.4	39	2	US-08-800-353-48	Sequence 48, App	C 663	9.6	53.3	20	4	US-08-946-914-46	Sequence 46, App
589	9.8	54.4	39	2	US-08-800-353-48	Sequence 48, App	C 664	9.6	53.3	20	4	US-08-946-914-46	Sequence 46, App
590	9.8	54.4	39	2	US-08-800-353-48	Sequence 48, App	C 665	9.6	53.3	20	4	US-08-946-914-46	Sequence 46, App
591	9.8	54.4	39	2	US-08-800-353-48	Sequence 48, App	C 666	9.6	53.3	20	4	US-08-946-914-46	Sequence 46, App
592	9.8	54.4	39	2	US-08-800-353-48	Sequence 48, App	C 667	9.6	53.3	20	4	US-08-946-914-46	Sequence 46, App
593	9.8	54.4	39	2	US-08-800-353-48	Sequence 48, App	C 668	9.6	53.3	20	4	US-08-946-914-46	Sequence 46, App
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597	9.8	54.4	39	2	US-08-800-353-48	Sequence 48, App	C 672	9.6	53.3	20	4	US-08-946-914-46	Sequence 46, App
598	9.8	54.4	39	2	US-08-800-353-48	Sequence 48, App	C 673	9.6	53.3	20	4	US-08-946-914-46	Sequence 46, App
599	9.8	54.4	39	2	US-08-800-353-48	Sequence 48, App	C 674	9.6	53.3	20	4	US-08-946-914-46	Sequence 46, App
600	9.8	54.4	39	2	US-08-800-353-48	Sequence 48, App	C 675	9.6	53.3	20	4	US-08-946-914-46	Sequence 46, App
601	9.8	54.4	39	2	US-08-800-353-48	Sequence 48, App	C 676	9.6	53.3	20	4	US-08-946-914-46	Sequence 46, App
602	9.8	54.4	39	2	US-08-800-353-48	Sequence 48, App	C 677	9.6	53.3	20	4	US-08-946-914-46	Sequence 46, App
603	9.8	54.4	39	2	US-08-800-353-48	Sequence 48, App	C 678	9.6	53.3	20	4	US-08-946-914-46	Sequence 46, App
604	9.8	54.4	39	2	US-08-800-353-48	Sequence 48, App	C 679	9.6	53.3	20	4	US-08-946-914-46	Sequence 46, App
605	9.8	54.4	39	2	US-08-800-353-48	Sequence 48, App	C 680	9.6	53.3	20	4	US-08-946-914-46	Sequence 46, App
606	9.8	54.4	39	2	US-08-800-353-48	Sequence 48, App	C 681	9.6	53.3	20	4	US-08-946-914-46	Sequence 46, App
607	9.8	54.4	39	2	US-08-800-353-48	Sequence 48, App	C 682	9.6	53.3	20	4	US-08-946-914-46	Sequence 46, App
608	9.8	54.4	39	2	US-08-800-353-48	Sequence 48, App	C 683	9.6	53.3	20	4	US-08-946-914-46	Sequence 46, App
609	9.8	54.4	39	2	US-08-800-353-48	Sequence 48, App	C 684	9.6	53.3	20	4	US-08-946-914-46	Sequence 46, App
610	9.8	54.4	39	2	US-08-800-353-48	Sequence 48, App							
611	9.6	53.3	17	3	US-08-310-259B-11	Sequence 11, App							
			16	3	US-09-344-520-13	Sequence 13, App							

665	9.6	53.3	35	4	US-09-352-654A-51	Sequence 51, Appl	C 758	9.6	53.3	50	2	US-08-635-761-26	Sequence 26, Appl
C 666	9.6	53.3	35	4	US-09-348-097-50	Sequence 50, Appl	C 759	9.6	53.3	50	2	US-08-635-761-27	Sequence 27, Appl
667	9.6	53.3	35	4	US-09-348-097-51	Sequence 51, Appl	C 760	9.6	53.3	50	2	US-08-635-761-28	Sequence 28, Appl
C 668	9.6	53.3	35	4	US-09-276-553A-8	Sequence 8, Appl	761	9.6	53.3	50	4	US-09-091-814-13	Sequence 13, Appl
669	9.6	53.3	36	4	US-09-250-580-3	Sequence 3, Appl	C 762	9.6	53.3	50	4	US-09-021-701-9	Sequence 9, Appl
670	9.6	53.3	37	1	US-08-591-452-17	Sequence 17, Appl	C 763	9.6	53.3	50	4	US-09-312-520-25	Sequence 25, Appl
C 671	9.6	53.3	37	3	US-08-938-830-57	Sequence 57, Appl	C 764	9.6	53.3	50	4	US-09-312-520-26	Sequence 26, Appl
C 672	9.6	53.3	37	3	US-08-858-003-13	Sequence 13, Appl	C 765	9.6	53.3	50	4	US-09-312-520-27	Sequence 27, Appl
C 673	9.6	53.3	37	3	US-09-078-166-13	Sequence 13, Appl	766	9.6	53.3	50	4	US-09-312-520-28	Sequence 28, Appl
C 674	9.6	53.3	37	4	US-08-997-467-13	Sequence 13, Appl	C 767	9.6	53.3	50	4	US-09-538-709-05	Sequence 95, Appl
675	9.6	53.3	38	1	US-08-106-078-5	Sequence 5, Appl	C 768	9.6	53.3	50	4	US-09-538-709-1262	Sequence 1262, Ap
C 676	9.6	53.3	38	1	US-08-591-492-5	Sequence 5, Appl	C 769	9.4	52.2	11	5	PCT-US94-05659-24	Sequence 24, Appl
677	9.6	53.3	38	2	US-08-276-967-4	Sequence 4, Appl	C 770	9.4	52.2	15	1	US-08-311-486C-172	Sequence 172, Ap
C 678	9.6	53.3	39	1	US-08-106-078-1	Sequence 1, Appl	C 771	9.4	52.2	15	2	US-08-292-620A-375	Sequence 375, Ap
699	9.6	53.3	39	1	US-08-631-200-6	Sequence 6, Appl	C 772	9.4	52.2	15	3	US-09-071-845-375	Sequence 375, Ap
700	9.6	53.3	39	1	US-08-591-492-1	Sequence 1, Appl	C 773	9.4	52.2	16	4	US-08-413-974-16	Sequence 16, Appl
701	9.6	53.3	39	1	US-08-829-553-6	Sequence 6, Appl	C 774	9.4	52.2	16	4	US-08-431-418-16	Sequence 16, Appl
702	9.6	53.3	39	2	US-08-922-267A-6	Sequence 6, Appl	C 775	9.4	52.2	16	4	US-08-433-288-16	Sequence 16, Appl
703	9.6	53.3	39	2	US-08-936-707A-6	Sequence 6, Appl	C 776	9.4	52.2	16	4	US-08-174-739A-16	Sequence 16, Appl
704	9.6	53.3	39	2	US-08-936-706A-6	Sequence 6, Appl	C 777	9.4	52.2	16	4	US-08-434-256-16	Sequence 16, Appl
705	9.6	53.3	39	3	US-09-248-203-6	Sequence 6, Appl	C 778	9.4	52.2	17	4	US-09-282-147-26	Sequence 26, Appl
C 706	9.6	53.3	39	3	US-09-091-348-14	Sequence 14, Appl	779	9.4	52.2	17	4	US-09-560-639-30	Sequence 30, Appl
C 707	9.6	53.3	39	4	US-09-406-071-6	Sequence 6, Appl	C 780	9.4	52.2	17	5	PCT-US91-03056-14	Sequence 14, Appl
C 708	9.6	53.3	40	2	US-08-596-387B-05	Sequence 65, Appl	C 781	9.4	52.2	18	1	US-08-647-584-12	Sequence 12, Appl
C 709	9.6	53.3	40	2	US-08-596-387B-66	Sequence 66, Appl	C 782	9.4	52.2	18	3	US-09-344-579-43	Sequence 43, Appl
C 710	9.6	53.3	40	4	US-09-067-615-65	Sequence 65, Appl	C 783	9.4	52.2	18	3	US-09-143-212-74	Sequence 74, Appl
711	9.6	53.3	40	4	US-09-067-615-66	Sequence 66, Appl	C 784	9.4	52.2	18	3	US-09-163-162-31	Sequence 31, Appl
C 712	9.6	53.3	40	5	PCT-US95-09816A-65	Sequence 65, Appl	C 785	9.4	52.2	18	4	US-09-286-407-31	Sequence 31, Appl
713	9.6	53.3	40	5	PCT-US95-09816A-66	Sequence 66, Appl	C 786	9.4	52.2	18	4	US-09-496-654B-40	Sequence 40, Appl
714	9.6	53.3	41	1	US-08-040-548-57	Sequence 57, Appl	C 787	9.4	52.2	18	4	US-09-696-654B-80	Sequence 80, Appl
715	9.6	53.3	41	1	US-08-466-344-57	Sequence 57, Appl	C 788	9.4	52.2	18	4	US-09-723-535-18	Sequence 18, Appl
C 716	9.6	53.3	41	2	US-08-781-620B-10	Sequence 10, Appl	C 789	9.4	52.2	19	1	US-08-605-089-11	Sequence 11, Appl
C 717	9.6	53.3	42	1	US-09-313-221A-28	Sequence 28, Appl	790	9.4	52.2	20	1	US-07-743-518-4	Sequence 4, Appl
718	9.6	53.3	42	1	US-08-137-117D-59	Sequence 59, Appl	791	9.4	52.2	20	1	US-07-743-518-9	Sequence 9, Appl
C 719	9.6	53.3	42	1	US-08-436-717-59	Sequence 59, Appl	792	9.4	52.2	20	1	US-07-977-284A-112	Sequence 112, Ap
C 720	9.6	53.3	43	1	US-08-578-649-15	Sequence 15, Appl	793	9.4	52.2	20	1	US-08-250-866A-33	Sequence 33, Appl
C 721	9.6	53.3	43	1	US-08-471-791-37	Sequence 37, Appl	794	9.4	52.2	20	1	US-08-271-880A-183	Sequence 183, Ap
722	9.6	53.3	44	4	US-09-142-334-14	Sequence 14, Appl	C 795	9.4	52.2	20	2	US-08-741-096-9	Sequence 9, Appl
C 723	9.6	53.3	44	5	PCT-US91-01746-37	Sequence 37, Appl	796	9.4	52.2	20	2	US-08-411-098-37	Sequence 37, Appl
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725	9.6	53.3	45	1	US-08-459-310-6	Sequence 6, Appl	798	9.4	52.2	20	2	US-08-256-426B-112	Sequence 112, Ap
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754	9.6	53.3	50	1	US-08-412-614-28	Sequence 28, Appl	C 827	9.4	52.2	20	5	PCT-US95-07111A-33	Sequence 33, Appl
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C 836	9.4	52.2	21	4	US-08-968-733-28	Sequence 28, Appl	909	9.4	52.2	38	3	US-09-071-845-2087	Sequence 2087, Ap
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ALIGNMENTS

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RESULT 1
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: Sequence 7, Application US/08447179
: Patent No. 5744303
: GENERAL INFORMATION:
: APPLICANT: Iggo, Richard
: APPLICANT: Friend, Stephen H.
: APPLICANT: Frebourg, Thierry
: APPLICANT: Ishioke, Chikashi
: TITLE OF INVENTION: FUNCTIONAL ASSAY FOR TUMOR
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson
: STREET: 225 Franklin Street
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: U.S.A.
: ZIP: 02110-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
: COMPUTER: IBM PS/2 Model 502 or 555X
: OPERATING SYSTEM: MS-DOS (Version 5.0)
: SOFTWARE: WordPerfect (Version 5.1)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/447,179
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/046,033
: FILING DATE: 12 APRIL 1993
: APPLICATION NUMBER: 07/956,696
: FILING DATE: 10 OCTOBER 1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Clark, Paul T.
: REGISTRATION NUMBER: 30,162
: REFERENCE/DOCKET NUMBER: 00786/159002
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 542-8906
: TELEFAX: (617) 542-5070
: TELEX: 200154
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 25

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: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
US-08-447-179-7

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Query Match 83.3%; Score 15; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 25 GGAAGCGAGCTGGC 11

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RESULT 2
US-08-363-240A-1088/c
: Sequence 1088, Application US/08363240A
: Patent No. 5705388
: GENERAL INFORMATION:
: APPLICANT: Couture, Larry
: APPLICANT: McSwiggen, James
: APPLICANT: Bisgaier, Charles
: APPLICANT: Pape, Michael
: TITLE OF INVENTION: METHOD AND REAGENT FOR
: TITLE OF INVENTION: PREVENTION, INHIBITION OF
: TITLE OF INVENTION: PROGRESSION AND REGRESSION
: TITLE OF INVENTION: OF VASCULAR DISEASES
: NUMBER OF SEQUENCES: 1243
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Lyon & Lyon
: STREET: 633 West Fifth Street
: STREET: Suite 4700
: CITY: Los Angeles
: STATE: California
: COUNTRY: U.S.A.
: ZIP: 90071
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
: MEDIUM TYPE: storage
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: IBM P.C. DOS 5.0
: SOFTWARE: Word Perfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/363,240A
: FILING DATE: December 23, 1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Warburg, Richard
: REGISTRATION NUMBER: 32,327
: REFERENCE/DOCKET NUMBER: 210/096
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (213) 489-1600
: TELEFAX: (213) 955-0440
: TELEX: 67-3510
: INFORMATION FOR SEQ ID NO: 1088:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 18 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
US-08-363-240A-1088

```

```

Query Match 71.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 6.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 2 CCGAAGCGAGCTGG 17
Db 16 CTGAAGCGAGCTGG 1

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;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/363,240A
;; FILING DATE: December 23, 1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 210/096
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; INFORMATION FOR SEQ ID NO: 1183:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-363-240A-1183

Query Match 68.9%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 GGAAGGAGCTCTGG 17
||| ||| ||| ||| |||
DB 18 GGAAGGAGCTCTGG 5

RESULT 6
US-09-243-335-22/c
; Sequence 22, Application US/09243335A
; Patent No. 6197580
; GENERAL INFORMATION:
; APPLICANT: American Home Products Corp.
; APPLICANT: Susulic, Vedrana S.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION OF THE HUMAN
; TITLE OF INVENTION: B3-ADRENERGIC RECEPTOR GENE
; FILE REFERENCE: 0630/0E791
; CURRENT APPLICATION NUMBER: US/09/243,335A
; CURRENT FILING DATE: 1999-02-01
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
US-09-243-335-22

Query Match 68.9%; Score 12.4; DB 4; Length 26;
Best Local Similarity 92.9%; Pred. No. 1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 GAAGGAGCTCTGG 18
||| ||| ||| ||| |||
DB 24 GAAGGAGCTCTGG 11

RESULT 7
US-09-593-589-37/c
; Sequence 37, Application US/09593589
; Patent No. 6306655
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF C/EBP ALPHA EXPRESSION
; FILE REFERENCE: RTS-0119

;; CURRENT APPLICATION NUMBER: US/09/593,589
;; CURRENT FILING DATE: 2000-06-13
;; NUMBER OF SEQ ID NOS: 94
;; SEQ ID NO 37
;; LENGTH: 20
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Antisense Oligonucleotide
US-09-593-589-37

Query Match 67.8%; Score 12.2; DB 4; Length 20;
Best Local Similarity 82.4%; Pred. No. 1.3e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CCCGAGGAGCTCTGG 17
||| ||| ||| ||| |||
DB 17 CCTGAGCGGAGCTGG 1

RESULT 8
US-08-442-010-12
; Sequence 12, Application US/08442010
; Patent No. 5849994
; GENERAL INFORMATION:
; APPLICANT: NARAYAN, Opendra
; TITLE OF INVENTION: Animal Model for HIV-1 Induced Disease
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & WITCOFF, Ltd.
; STREET: 10 S. Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,010
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: CHAO, MARK
; REGISTRATION NUMBER: 37,293
; REFERENCE/DOCKET NUMBER: 95,645
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)715-1234
; TELEFAX: (312)715-1234
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "PCR primer"
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: 1..26
; OTHER INFORMATION: /note= "complementary to B-actin"
; OTHER INFORMATION: gene"
US-08-442-010-12

Query Match 67.8%; Score 12.2; DB 2; Length 26;
Best Local Similarity 82.4%; Pred. No. 1.3e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CCCGAGGAGCTCTGG 17
||| ||| ||| ||| |||
DB 1 CCGAGGAGGAGCTGG 17

RESULT 9
546668-50/c
; Patent No. 546668
; APPLICANT: GLASER, CHARLES B.; MORSE, MICHAEL J.; LIGHT,
; DAVID R.
; TITLE OF INVENTION: SUPERIOR THROMBOMODULIN ANALOGS FOR
; PHARMACEUTICAL USE
; NUMBER OF SEQUENCES: 57
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/155,346
; FILING DATE: 22-NOV-1993
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 568,456
; FILING DATE: 15-AUG-1990
; APPLICATION NUMBER: 506,325
; FILING DATE: 09-APR-1990
; APPLICATION NUMBER: 406,941
; FILING DATE: 13-SEP-1989
; APPLICATION NUMBER: 345,374
; FILING DATE: 28-APR-1989
; SEQ ID NO: 50:
; LENGTH: 28
546668-50

Query Match
Best Local Similarity 67.8%; Score 12.2; DB 6; Length 28;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCGGAGCAGCTCTGGC 18
Db 18 CCGGTACGACGCTCTGGC 2

RESULT 10
US-08-780-949-2/c
; Sequence 2, Application US/08780949
; Patent No. 6002066
; GENERAL INFORMATION:
; APPLICANT: Leung, Wei-Ping
; APPLICANT: Karlsson, Lars
; APPLICANT: Zhou, Lubing
; APPLICANT: Peterson, Per A.
; TITLE OF INVENTION: H2-M MODIFIED TRANSGENIC ANIMALS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Johnson & Johnson
; STREET: One Johnson & Johnson Plaza
; CITY: New Brunswick
; STATE: NJ
; COUNTRY: USA
; ZIP: 08933-7003
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,949
; FILING DATE: 10 January 1997
; CLASSIFICATION: 8B0
; ATTORNEY/AGENT INFORMATION:
; NAME: Mallen, John W.
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: OBT-819
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-524-2806
; TELEFAX: 732-524-2808
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid

STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; ANTI-SENSE: NO
US-08-780-949-2

Query Match
Best Local Similarity 66.7%; Score 12; DB 3; Length 23;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AAGCAGCTCTGG 17
Db 23 AAGCAGCTCTGG 12

RESULT 11
US-08-881-038A-1/c
; Sequence 1, Application US/08881038A
; Patent No. 6110902
; GENERAL INFORMATION:
; APPLICANT: Mohler, Hans
; APPLICANT: Bolson, Detlev
; TITLE OF INVENTION: METHODS FOR THE INHIBITION
; OF NEURONAL ACTIVITY BY LOCAL DELIVERY OF ADENOSINE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 115 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,038A
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Friebe, Thomas E.
; REGISTRATION NUMBER: 29,258
; REFERENCE/DOCKET NUMBER: 9261-0003-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-881-038A-1

Query Match
Best Local Similarity 66.7%; Score 12; DB 3; Length 26;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AAGCAGCTCTGG 17
Db 17 AAGCAGCTCTGG 6

RESULT 12
US-08-231-990-34/c
; Sequence 34, Application US/08231990
; Patent No. 5585232

```

; GENERAL INFORMATION:
; APPLICANT: Fair, Spencer B
; TITLE OF INVENTION: METHODS AND DIAGNOSTIC KITS FOR
; TITLE OF INVENTION: DETERMINING TOXICITY
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 875 Third Avenue - 29th Floor
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,990
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/910,793
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr, James F
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: Paritox-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 715-0600
; TELEFAX: (212) 715-0673
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-231-990-34
;
Query Match 65.6%; Score 11.8; DB 1; Length 21;
Best Local Similarity 86.7%; Pred. No. 2.1e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
QY 1 CCCGGAAGCAGCTCT 15
Db 19 CCCGGAAGCGGTTT 5
;
RESULT 13
US-08-367-122-34/c
; Sequence 34, Application US/08367122
; Patent No. 5589337
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: METHODS AND DIAGNOSTIC KITS FOR
; TITLE OF INVENTION: DETERMINING TOXICITY UTILIZING BACTERIAL STRESS
; TITLE OF INVENTION: PROMOTERS FUSED TO REPORTER GENES
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/367,122
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06537
; FILING DATE: 06-JUL-1993
; APPLICATION NUMBER: US 07/910,793
; FILING DATE: 06-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Marks, Andrew S.
; REGISTRATION NUMBER: 33,259
; REFERENCE/DOCKET NUMBER: Paritox-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-367-122-34
;
Query Match 65.6%; Score 11.8; DB 1; Length 21;
Best Local Similarity 86.7%; Pred. No. 2.1e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
QY 1 CCCGGAAGCAGCTCT 15
Db 19 CCCGGAAGCGGTTT 5
;
RESULT 14
US-09-632-098-7
; Sequence 7, Application US/09632098
; Patent No. 6420154
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Balindur, Nand
; TITLE OF INVENTION: MAMMALIAN ADHESION PROTEASE PEPTIDES
; FILE REFERENCE: 99-39
; CURRENT APPLICATION NUMBER: US/09/632,098
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide ZC17,993
; US-09-632-098-7
;
Query Match 65.6%; Score 11.8; DB 4; Length 23;
Best Local Similarity 86.7%; Pred. No. 2.1e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
QY 1 CCCGGAAGCAGCTCT 15
Db 7 CCTGGAAGCAGTCTT 21
;
RESULT 15
US-09-199-637A-178
; Sequence 178, Application US/09199637A
; Patent No. 6355411
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick
; APPLICANT: Goodman, Howard M.
; APPLICANT: Rahme, Laurence G.
; APPLICANT: Mahajan-Miklos, Shalina

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; APPLICANT: Tan, Man-Wah
; APPLICANT: Cao, Hui
; APPLICANT: Drenkard, Eliana
; APPLICANT: Tsongalis, John
; TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
; FILE REFERENCE: 00786/361002
; CURRENT APPLICATION NUMBER: US/09/199,637A
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-178

Query Match
Best Local Similarity 86.7%; Score 11.8; DB 4; Length 24;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCGGAGCGACTGCTG 16
Db 9 CCGGAGCGAGCTGCTG 23

RESULT 16
US-07-885-689A-22/C
; Sequence 22, Application US/07885689A
; Patent No. 5366876
; GENERAL INFORMATION:
; APPLICANT: Cho, Joong M.
; APPLICANT: Lee, Tae H.
; APPLICANT: Chung, Hyun H.
; APPLICANT: Lee, Yong B.
; APPLICANT: Lee, Tae G.
; APPLICANT: Park, Young W.
; APPLICANT: Han, Kyu B.
; TITLE OF INVENTION: Method for Production of Bovine Growth
; TITLE OF INVENTION: Hormone Using a Synthetic Gene.
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolash & Birch
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/885,689A
; FILING DATE: 19-MAY-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30,330
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
```

```

; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; FEATURE:
; NAME/KEY:
; LOCATION: 1..45
; OTHER INFORMATION: /label= oligonucleotide
; OTHER INFORMATION: /note= "L9 oligonucleotide portion of synthetic
; OTHER INFORMATION: Bch gene, Figure 1."
US-07-885-689A-22

Query Match
Best Local Similarity 86.7%; Score 11.8; DB 1; Length 45;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGAAGCGACTCTGCG 18
Db 20 GGAAGCGACTCTGCG 6

RESULT 17
US-09-253-396A-113
; Sequence 113, Application US/09253396A
; Patent No. 6205404
; GENERAL INFORMATION:
; APPLICANT: Genome Dynamics, Inc.
; TITLE OF INVENTION: DNA-Binding proteins of the Zinc-Finger Class
; FILE REFERENCE: 1116242-0003 file: genome03f.app
; CURRENT APPLICATION NUMBER: US/09/253,396A
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 113
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
US-09-253-396A-113

Query Match
Best Local Similarity 77.8%; Score 11.6; DB 4; Length 27;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCGGAGCGACTGCTGCG 18
Db 1 CCGGAGCGCGACTGCG 18

RESULT 18
US-08-840-062-12/C
; Sequence 12, Application US/08840062
; Patent No. 6119777
; GENERAL INFORMATION:
; APPLICANT: LASKY, LAURENCE A.
; APPLICANT: WU, KAI
; TITLE OF INVENTION: TYPE C LECTINS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/840,062
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dregler, Ginger R.
```

REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1019R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-840-062-12

Query Match 64.4%; Score 11.6; DB 3; Length 29;
Best Local Similarity 77.8%; Pred. No. 2.6e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CCGGAGGCGAGCTGGC 18
DB 23 CCGGAGGCGAGCGAGC 6

RESULT 19
US-09-732-199A-22/c
Sequence 22, Application US/09732199A
Patent No. 6379960
GENERAL INFORMATION:
APPLICANT: Ian Popoff
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF DAMAGE-SPECIFIC DNA BINDING PROTEIN 2, P4
FILE REFERENCE: RTS-0214
CURRENT APPLICATION NUMBER: US/09/732,199A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 57
SEQ ID NO 22
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-732-199A-22

Query Match 63.3%; Score 11.4; DB 4; Length 20;
Best Local Similarity 92.3%; Pred. No. 3.2e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 AAGCAGCTCTGGC 18
DB 16 AAGCAGCGCTGGC 4

RESULT 20
US-08-370-724-6/c
Sequence 6, Application US/08370724
Patent No. 5972598
GENERAL INFORMATION:
APPLICANT: Chaudhary, Preet
APPLICANT: Shull, Alexander
APPLICANT: Roninson, Igor B.
TITLE OF INVENTION: Methods for Preventing Multidrug
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 S. Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,724
FILING DATE: 09-JAN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: No. 5972598nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 95,119
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-370-724-6

Query Match 63.3%; Score 11.4; DB 2; Length 21;
Best Local Similarity 92.3%; Pred. No. 3.2e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 GAGCAGCTCTGG 17
DB 16 GAGGAGAGCTGG 4

RESULT 21
US-08-659-877-6/c
Sequence 6, Application US/08659877
Patent No. 6171786
GENERAL INFORMATION:
APPLICANT: Shull, Alexander
APPLICANT: Roninson, Igor B.
TITLE OF INVENTION: Methods for Preventing Multidrug Resistance
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 S. Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,877
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 6171786nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 95,119-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

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; MOLECULE TYPE: DNA (genomic)
; US-08-659-877-6
Query Match      63.3%; Score 11.4; DB 4; Length 21;
Best Local Similarity 92.3%; Pred. No. 3.2e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 GAAGCAGCTCTGC 17
        |||||
DB      16 GAAGCAGCTCTGC 4

RESULT 22
US-08-328-314-7
; Sequence 7, Application US/08328314
; Patent No. 5674728
; GENERAL INFORMATION:
; APPLICANT: Buxton, Frank
; APPLICANT: Jarai, Gabor
; APPLICANT: Visser, Jacob
; TITLE OF INVENTION: Fungal Protease
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,314
; FILING DATE: TBA
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Spurrill, W. Murray
; REGISTRATION NUMBER: .32,943
; REFERENCE/DOCKET NUMBER: 4-19746/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8615
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..28
; OTHER INFORMATION: /standard_name= "oligonucleotide 5"

; US-08-328-314-7
Query Match      63.3%; Score 11.4; DB 1; Length 28;
Best Local Similarity 92.3%; Pred. No. 3.3e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AAGCAGCTCTGC 18
        |||||
DB      16 AAGCAGCTCTGC 28

RESULT 23
US-08-731-045-7
; Sequence 7, Application US/08731045
; Patent No. 5756338
; GENERAL INFORMATION:
; APPLICANT: Buxton, Frank
```

```
; APPLICANT: Jarai, Gabor
; APPLICANT: Visser, Jacob
; TITLE OF INVENTION: Fungal Protease
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY CORPORATION
; STREET: 520 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9725
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/731,045
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: 08/328,314
; APPLICATION NUMBER: 08/328,314
; FILING DATE: October 24, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 4-19746/A/DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-3318
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..28
; OTHER INFORMATION: /standard_name= "oligonucleotide 5"

; US-08-731-045-7
Query Match      63.3%; Score 11.4; DB 1; Length 28;
Best Local Similarity 92.3%; Pred. No. 3.3e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 AAGCAGCTCTGC 18
        |||||
DB      16 AAGCAGCTCTGC 28

RESULT 24
US-08-385-191A-7/C
; Sequence 7, Application US/08385191A
; Patent No. 5821078
; GENERAL INFORMATION:
; APPLICANT: COHEN, Batya
; APPLICANT: NOVICK, Daniela
; APPLICANT: RUBINSTEIN, Menachem
; TITLE OF INVENTION: INTERFERON-ALPHA/BETA BINDING PROTEIN,
; TITLE OF INVENTION: ITS PREPARATION AND USE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NETMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
```

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;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentln Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/385,191A
;; FILING DATE: 07-FEB-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/115,741
;; FILING DATE: 03-SEP-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BROWDY, Roger L.
;; REGISTRATION NUMBER: 25,618
;; REFERENCE/DOCKET NUMBER: NOVICK=7A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 38 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: CDNA
;; US-08-385-191A-7
```

```
Query Match      63.3%; Score 11.4; DB 1; Length 38;
Best Local Similarity 92.3%; Pred. No. 3.4e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy      6 AAGCAGCTCTGCG 18
        ||||| |||||
Db      38 AAGCATTCTGCG 26
```

```
RESULT 25
US-08-472-402A-7/c
; Sequence 7, Application US/08472402A
; Patent No. 6458932
; GENERAL INFORMATION:
; APPLICANT: COHEN, Batya
; APPLICANT: NOVICK, Daniela
; APPLICANT: RUBINSTEIN, Menachem
; TITLE OF INVENTION: INTERFERON-ALPHA/BETA BINDING PROTEIN,
; TITLE OF INVENTION: ITS PREPARATION AND USE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,402A
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/385,191
; FILING DATE: 07-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/115,741
; FILING DATE: 03-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: NOVICK=7B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 7:
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```
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 38 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: CDNA
;; US-08-472-402A-7
```

```
Query Match      63.3%; Score 11.4; DB 4; Length 38;
Best Local Similarity 92.3%; Pred. No. 3.4e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy      6 AAGCAGCTCTGCG 18
        ||||| |||||
Db      38 AAGCATTCTGCG 26
```

```
RESULT 26
US-09-418-640-57
; Sequence 57, Application US/09418640
; Patent No. 6140125
; GENERAL INFORMATION:
; APPLICANT: Jennifer K. Taylor
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL-6 EXPRESSION
; FILE REFERENCE: RTS-0102
; CURRENT APPLICATION NUMBER: US/09/418,640
; CURRENT FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 57
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-418-640-57
```

```
Query Match      62.2%; Score 11.2; DB 3; Length 20;
Best Local Similarity 81.2%; Pred. No. 4e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Oy      3 CGGAGGCGCTGCG 18
        ||||| | |||||
Db      4 CGGAGGAGGCGCTGCG 19
```

```
RESULT 27
US-09-109-663-15
; Sequence 15, Application US/09109663
; Patent No. 6277981
; GENERAL INFORMATION:
; APPLICANT: Tu, Guang-Chou
; APPLICANT: Israel, Yedy
; TITLE OF INVENTION: AN IMPROVED METHOD FOR DESIGN AND SELECTION OF
; TITLE OF INVENTION: EFFICACIOUS ANTISENSE OLIGONUCLEOTIDES
; FILE REFERENCE: 9855-301
; CURRENT APPLICATION NUMBER: US/09/109,663
; CURRENT FILING DATE: 1998-07-03
; EARLIER APPLICATION NUMBER: 60/051,705
; EARLIER FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Candidate
; OTHER INFORMATION: TNF(alpha) ASO
US-09-109-663-15
```

```
Query Match      62.2%; Score 11.2; DB 4; Length 20;
Best Local Similarity 81.2%; Pred. No. 4e+03;
```


OY 2 CCGAAGCGAGTCTGG 17
| | | | | | | | | |
DB 25 CTGAAGCGCATCTCTG 10

RESULT 32

US-09-263-944-12/c
; Sequence 12, Application US/09263944
; Patent No. 6251602

GENERAL INFORMATION:

APPLICANT: Young, Kathleen H.
APPLICANT: Ozenberger, Bradley A.
TITLE OF INVENTION: No. 6251602el Cell System Having Specific
TITLE OF INVENTION: Interaction of Peptide Binding Pairs
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,944
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,609
FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Webster, Darryl L.
REGISTRATION NUMBER: 34,276
REFERENCE/DOCKET NUMBER: 32,352-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3247
TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-263-944-12

Query Match Best Local Similarity 62.2%; Score 11.2; DB 4; Length 27;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 CCGAAGCGAGTCTGG 17
| | | | | | | | | |
DB 25 CTGAAGCGCATCTCTG 10

RESULT 33
US-09-305-483-12/c
; Sequence 12, Application US/09305483
; Patent No. 6284519

GENERAL INFORMATION:

APPLICANT: Young, Kathleen H.
APPLICANT: Ozenberger, Bradley A.
TITLE OF INVENTION: No. 6284519el Cell System Having Specific
TITLE OF INVENTION: Interaction of Peptide Binding Pairs
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza

CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/305,483
FILING DATE: 06-MAY-1999

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/259,609
FILING DATE: 14-JUN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Webster, Darryl L.
REGISTRATION NUMBER: 34,276
REFERENCE/DOCKET NUMBER: 32,352-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3247
TELEFAX: 201-831-3305

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-305-483-12

Query Match Best Local Similarity 62.2%; Score 11.2; DB 4; Length 27;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 CCGAAGCGAGTCTGG 17
| | | | | | | | | |
DB 25 CTGAAGCGCATCTCTG 10

RESULT 34
US-08-446-660-7/c
; Sequence 7, Application US/08446660
; Patent No. 5723328

GENERAL INFORMATION:

APPLICANT: Dalboege, Henrik
APPLICANT: Andersen, Lene N
APPLICANT: Koefed, Lene V
APPLICANT: Kauppinen, Markus S
APPLICANT: Christgau, Stephan
TITLE OF INVENTION: AN ENZYME WITH ENDOGLUCANASE ACTIVITY
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 57233280 No. 57233280disk of No. 57233280th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,660
FILING DATE: 26-MAY-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 3950.204-US
TELECOMMUNICATION INFORMATION:

ADDRESS: Flehr, Hohbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/604,165
FILING DATE: 21-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9503395.7
FILING DATE: 21-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9515557.8
FILING DATE: 28-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9603322.0
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Linda R. Judge
REGISTRATION NUMBER: 42,702
REFERENCE/DOCKET NUMBER: A-63282/WHD/LRJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 871-1989
TELEFAX: (415) 949-8711
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-604-165-10

Query Match 62.2%; Score 11.2; DB 4; Length 29;
Best Local Similarity 81.2%; Pred. No. 4.1e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCGAGGCACTCTG 16
DB 17 CCCGAGCAATCTG 2

RESULT 38
US-08-734-054B-10/C
Sequence 10, Application US/08734054B
Patent No. 6344445
GENERAL INFORMATION:
APPLICANT: BOURSNEILL, Michael E.G.
APPLICANT: BRENNER, Malcolm K.
APPLICANT: DILLOO, Dagmar
APPLICANT: INGILIS, Stephen C.
TITLE OF INVENTION: Herpes Virus Vectors and Their Uses
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/734,054B
FILING DATE: 18-OCT-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,649
FILING DATE: 19-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Dregler, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-64068/WHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-734-054B-10

Query Match 62.2%; Score 11.2; DB 4; Length 29;
Best Local Similarity 81.2%; Pred. No. 4.1e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCGAGGCACTCTG 16
DB 17 CCCGAGCAATCTG 2

RESULT 39
US-08-974-549A-625
Sequence 625, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morlin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 625:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY:
; LOCATION: 1..32
; OTHER INFORMATION: /note="reverse01 primer"
; US-08-974-549A-625

Query Match      62.2%; Score 11.2; DB 4; Length 32;
Best Local Similarity 81.2%; Pred. No. 4.2e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CCGAAGGAGCTCTG 17
        |||||  |||||
Db      11 CCGAAGAGTGTCTG 26

RESULT 40
US-09-560-367A-17
; Sequence 17, Application US/09560367A
; Patent No. 6410301
; GENERAL INFORMATION:
; APPLICANT: Kusan Pharmaceuticals, Inc.
; APPLICANT: Julien, Bryan
; APPLICANT: Katz, Leonard
; APPLICANT: Khosla, Chaitan
; TITLE OF INVENTION: LIBRARY OF NOVEL "UNNATURAL" NATURAL PRODUCTS
; FILE REFERENCE: 30062-20031.20
; CURRENT APPLICATION NUMBER: US/09/560,367A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 09/443,501
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: PCT/US 99/27438
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: US 60/130,560
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 60/122,620
; PRIOR FILING DATE: 1999-03-03
; PRIOR APPLICATION NUMBER: US 60/119,386
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/109,401
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; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer 90-106
; US-09-560-367A-17

Query Match      62.2%; Score 11.2; DB 4; Length 32;
Best Local Similarity 81.2%; Pred. No. 4.2e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CCCGAGGAGCTCTG 16
        |||||  ||
Db      13 CCCGAGGAGCTCTG 28

Search completed: December 2, 2002, 14:07:11
Job time : 64 secs
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 2, 2002, 13:33:48 ; Search time 51 Seconds
(without alignments)
135.923 Million cell updates/sec

Title: US-09-848-868-35

Perfect score: 18

Sequence: 1 cccggaagcagctcggc 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 341543 seqs, 19255720 residues

Total number of hits satisfying chosen parameters: 177872

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	11.8	65.6	17	10 US-09-866-108-1471	Sequence 1472, Ap
5	11.8	65.6	17	10 US-09-866-108-1472	Sequence 1473, Ap
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7	11.8	65.6	25	10 US-09-866-108-4400	Sequence 4400, Ap
8	11.8	65.6	25	10 US-09-866-108-4401	Sequence 4401, Ap
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19	11.6	64.4	22	10 US-09-769-207A-15	Sequence 15, Appl

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21	11.6	64.4	45	10 US-09-780-669-942	Sequence 942, App
22	11.6	64.4	45	10 US-09-822-827-942	Sequence 942, App
23	11.4	63.3	28	10 US-09-825-414-81	Sequence 81, Appl
24	11.4	63.3	36	10 US-09-870-203A-25	Sequence 25, Appl
25	11.4	63.3	36	10 US-09-870-203A-26	Sequence 26, Appl
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28	11.2	62.2	21	10 US-09-846-373B-7	Sequence 7, Appl1
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34	11.2	62.2	36	10 US-09-870-203A-29	Sequence 29, Appl
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36	11.2	62.2	46	10 US-09-908-599-19	Sequence 21, Appl
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66	10.8	60.0	42	10 US-09-910-120-58	Sequence 249, App
67	10.8	60.0	47	9 US-09-853-525-249	Sequence 326, App
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82	10.4	57.8	23	10 US-10-039-785-7	Sequence 34, Appl
83	10.4	57.8	31	10 US-09-801-274-82	Sequence 82, Appl
84	10.4	57.8	31	10 US-09-801-274-82	Sequence 82, Appl
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c 102	10.2	56.7	20	10	US-09-759-984-3	Sequence 3, Appl	175	10	55.6	24	10	US-09-989-732-451	Sequence 451, App
c 103	10.2	56.7	20	10	US-09-989-722-17	Sequence 17, Appl	176	10	55.6	24	10	US-09-989-732-451	Sequence 451, App
c 104	10.2	56.7	20	10	US-09-989-723-17	Sequence 17, Appl	177	10	55.6	24	10	US-09-989-732-451	Sequence 451, App
c 105	10.2	56.7	20	10	US-09-989-727-17	Sequence 17, Appl	178	10	55.6	24	10	US-09-989-732-451	Sequence 451, App
c 106	10.2	56.7	20	10	US-09-989-727-17	Sequence 17, Appl	179	10	55.6	24	10	US-09-989-732-451	Sequence 451, App
c 107	10.2	56.7	20	10	US-09-989-727-17	Sequence 17, Appl	180	10	55.6	24	10	US-09-989-732-451	Sequence 451, App
c 108	10.2	56.7	20	10	US-09-859-291-5	Sequence 5, Appl	181	10	55.6	24	10	US-09-989-732-451	Sequence 451, App
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c 114	10.2	56.7	20	10	US-09-990-442-17	Sequence 17, Appl	187	10	55.6	25	10	US-09-866-108-11167	Sequence 11167, A
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c 131	10.2	56.7	25	10	US-09-866-108-14126	Sequence 14126, A	204	10	55.6	25	10	US-09-866-108-12171	Sequence 12171, A
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c 139	10.2	56.7	28	10	US-09-452-599-125	Sequence 125, App	212	10	55.6	25	10	US-09-866-108-14135	Sequence 14135, A
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c 143	10.2	56.7	30	10	US-09-795-483-14	Sequence 14, Appl	216	10	55.6	31	10	US-09-801-574-1128	Sequence 1128, Ap
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c 145	10.2	56.7	30	10	US-09-829-855-152	Sequence 152, App	218	10	55.6	32	10	US-09-814-777A-49	Sequence 49, Appl
c 146	10.2	56.7	31	10	US-09-801-274-709	Sequence 709, App	219	10	55.6	36	9	US-09-252-150-55	Sequence 55, Appl
c 147	10.2	56.7	32	10	US-09-750-373-30	Sequence 30, Appl	220	10	55.6	36	9	US-10-145-014-17	Sequence 17, Appl
c 148	10.2	56.7	33	10	US-09-754-532-64	Sequence 64, Appl	221	10	55.6	36	10	US-09-982-308-17	Sequence 17, Appl
c 149	10.2	56.7	36	9	US-10-037-677-14	Sequence 14, Appl	222	10	55.6	36	10	US-09-814-592-20	Sequence 20, Appl
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c 151	10.2	56.7	37	10	US-09-158-120A-15	Sequence 15, Appl	224	10	55.6	40	9	US-10-101-392-16	Sequence 16, Appl
c 152	10.2	56.7	38	10	US-09-870-203A-23	Sequence 23, Appl	225	10	55.6	40	9	US-10-101-392-18	Sequence 18, Appl
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c 156	10.2	56.7	45	10	US-09-780-669-782	Sequence 782, App	229	9.8	54.4	17	10	US-09-866-108-12215	Sequence 2215, Ap
c 157	10.2	56.7	45	10	US-09-822-827-782	Sequence 782, App	230	9.8	54.4	17	10	US-09-866-108-12262	Sequence 2262, Ap
c 158	10.2	56.7	46	10	US-09-216-393-362	Sequence 362, App	231	9.8	54.4	17	10	US-09-866-108-12263	Sequence 2263, Ap
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c 161	10	55.6	17	10	US-09-866-108-7272	Sequence 7272, Ap	234	9.8	54.4	17	10	US-09-866-108-12266	Sequence 2266, Ap
c 162	10	55.6	17	10	US-09-866-108-7273	Sequence 7273, Ap	235	9.8	54.4	17	10	US-09-817-014-137	Sequence 137, App
c 163	10	55.6	17	10	US-09-866-108-7274	Sequence 7274, Ap	236	9.8	54.4	18	10	US-09-565-233-1	Sequence 93, Appl
c 164	10	55.6	17	10	US-09-866-108-7275	Sequence 7275, Ap	237	9.8	54.4	19	9	US-10-104-019-33	Sequence 17, Appl
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241	9.8	54.4	19	10	US-09-950-046A-19	Sequence 19, Appl	314	9.6	53.3	21	10	US-09-989-732-455	Sequence 455, App
242	9.8	54.4	20	10	US-09-969-373-3083	Sequence 3083, Ap	315	9.6	53.3	21	10	US-09-991-073-455	Sequence 455, App
243	9.8	54.4	21	9	US-10-103-830-2	Sequence 2, Appl1	316	9.6	53.3	21	10	US-09-990-442-455	Sequence 455, App
244	9.8	54.4	21	10	US-09-733-444-4	Sequence 4, Appl1	317	9.6	53.3	21	10	US-09-991-163-455	Sequence 455, App
245	9.8	54.4	24	10	US-09-898-570-49	Sequence 49, Appl	318	9.6	53.3	21	10	US-09-993-604-455	Sequence 455, App
246	9.8	54.4	25	9	US-09-905-291A-329	Sequence 329, App	319	9.6	53.3	21	10	US-09-990-456-455	Sequence 455, App
247	9.8	54.4	25	10	US-09-564-329A-21	Sequence 21, Appl	320	9.6	53.3	21	10	US-09-989-721-455	Sequence 455, App
248	9.8	54.4	25	10	US-09-866-108-4397	Sequence 4397, Ap	321	9.6	53.3	23	10	US-09-909-320-411	Sequence 411, App
249	9.8	54.4	25	10	US-09-866-108-4411	Sequence 4411, Ap	322	9.6	53.3	23	10	US-09-909-320-411	Sequence 411, App
250	9.8	54.4	25	10	US-09-866-108-4119	Sequence 4119, Ap	323	9.6	53.3	23	10	US-09-909-320-411	Sequence 411, App
251	9.8	54.4	25	10	US-09-866-108-5152	Sequence 5152, Ap	324	9.6	53.3	24	9	US-09-875-440-6	Sequence 6, Appl1
252	9.8	54.4	25	10	US-09-866-108-5191	Sequence 5191, Ap	325	9.6	53.3	24	9	US-09-943-388-25	Sequence 25, Appl1
253	9.8	54.4	25	10	US-09-866-108-5192	Sequence 5192, Ap	326	9.6	53.3	24	10	US-09-946-175-32	Sequence 32, Appl
254	9.8	54.4	25	10	US-09-866-108-5193	Sequence 5193, Ap	327	9.6	53.3	25	10	US-09-866-108-11160	Sequence 11160, A
255	9.8	54.4	25	10	US-09-866-108-5194	Sequence 5194, Ap	328	9.6	53.3	25	10	US-09-866-108-11161	Sequence 11161, A
256	9.8	54.4	25	10	US-09-866-108-5195	Sequence 5195, Ap	329	9.6	53.3	25	10	US-09-866-108-12033	Sequence 12033, A
257	9.8	54.4	25	10	US-09-866-108-5196	Sequence 5196, Ap	330	9.6	53.3	25	10	US-09-866-108-12034	Sequence 12034, A
258	9.8	54.4	25	10	US-09-866-108-5197	Sequence 5197, Ap	331	9.6	53.3	25	10	US-09-866-108-12035	Sequence 12035, A
259	9.8	54.4	25	10	US-09-866-108-5198	Sequence 5198, Ap	332	9.6	53.3	25	10	US-09-866-108-12036	Sequence 12036, A
260	9.8	54.4	25	10	US-09-866-108-5199	Sequence 5199, Ap	333	9.6	53.3	25	10	US-09-866-108-12037	Sequence 12037, A
261	9.8	54.4	25	10	US-09-866-108-5200	Sequence 5200, Ap	334	9.6	53.3	25	10	US-09-866-108-12038	Sequence 12038, A
262	9.8	54.4	25	10	US-09-866-108-5201	Sequence 5201, Ap	335	9.6	53.3	25	10	US-09-866-108-12039	Sequence 12039, A
263	9.8	54.4	25	10	US-09-866-108-5202	Sequence 5202, Ap	336	9.6	53.3	25	10	US-09-866-108-12040	Sequence 12040, A
264	9.8	54.4	25	10	US-09-866-108-5203	Sequence 5203, Ap	337	9.6	53.3	25	10	US-09-866-108-12041	Sequence 12041, A
265	9.8	54.4	25	10	US-09-828-447-37	Sequence 37, Appl	338	9.6	53.3	25	10	US-09-866-108-14137	Sequence 14137, A
266	9.8	54.4	25	10	US-09-855-153-21	Sequence 21, Appl	339	9.6	53.3	25	10	US-09-866-108-14138	Sequence 14138, A
267	9.8	54.4	25	10	US-09-909-320-329	Sequence 21, Appl	340	9.6	53.3	25	10	US-09-263-689-46	Sequence 46, Appl
268	9.8	54.4	25	10	US-09-934-773-21	Sequence 21, Appl	341	9.6	53.3	25	10	US-09-263-689-46	Sequence 46, Appl
269	9.8	54.4	25	10	US-09-963-620-21	Sequence 21, Appl	342	9.6	53.3	25	10	US-09-263-689-46	Sequence 46, Appl
270	9.8	54.4	25	10	US-09-909-088B-329	Sequence 129, Appl	343	9.6	53.3	26	10	US-09-263-689-46	Sequence 46, Appl
271	9.8	54.4	26	10	US-09-564-329A-24	Sequence 24, Appl	344	9.6	53.3	26	10	US-09-886-404-16	Sequence 16, Appl
272	9.8	54.4	26	10	US-09-855-153-24	Sequence 24, Appl	345	9.6	53.3	27	10	US-09-817-014-84	Sequence 84, Appl
273	9.8	54.4	26	10	US-09-854-811-24	Sequence 24, Appl	346	9.6	53.3	29	10	US-09-817-014-84	Sequence 84, Appl
274	9.8	54.4	26	10	US-09-934-773-24	Sequence 24, Appl	347	9.6	53.3	31	10	US-09-922-261-35	Sequence 35, Appl
275	9.8	54.4	26	10	US-09-963-620-24	Sequence 24, Appl	348	9.6	53.3	31	10	US-09-864-864-170	Sequence 170, Appl
276	9.8	54.4	26	10	US-09-934-773-24	Sequence 24, Appl	349	9.6	53.3	31	10	US-09-801-274-57	Sequence 57, Appl
277	9.8	54.4	26	10	US-09-729-674-228	Sequence 228, Appl	350	9.6	53.3	31	10	US-09-801-274-1138	Sequence 1138, Ap
278	9.8	54.4	31	10	US-09-801-274-230	Sequence 230, App	351	9.6	53.3	31	10	US-09-801-274-1274	Sequence 1274, Ap
279	9.8	54.4	31	10	US-09-801-274-231	Sequence 231, App	352	9.6	53.3	36	10	US-09-801-274-1274	Sequence 1274, Ap
280	9.8	54.4	31	10	US-09-801-274-411	Sequence 411, App	353	9.6	53.3	36	10	US-09-245-487B-27	Sequence 27, Appl
281	9.8	54.4	31	10	US-09-801-274-1333	Sequence 1333, Ap	354	9.6	53.3	36	10	US-09-946-175-33	Sequence 33, Ap
282	9.8	54.4	31	10	US-09-801-274-1401	Sequence 1401, Ap	355	9.6	53.3	36	10	US-09-870-203A-28	Sequence 28, Appl
283	9.8	54.4	32	10	US-09-738-396-32	Sequence 32, Appl	356	9.6	53.3	36	10	US-09-870-203A-28	Sequence 28, Appl
284	9.8	54.4	36	9	US-10-085-519-14	Sequence 14, Appl	357	9.6	53.3	39	10	US-09-937-502-1	Sequence 1, Appl1
285	9.8	54.4	38	10	US-09-758-269-21	Sequence 21, Appl	358	9.6	53.3	39	10	US-09-814-986-6	Sequence 6, Appl1
286	9.8	54.4	39	9	US-09-907-900-18	Sequence 18, Appl	359	9.6	53.3	40	10	US-09-027-439-33	Sequence 33, Appl
287	9.8	54.4	39	10	US-09-855-797A-18	Sequence 18, Appl	360	9.6	53.3	40	10	US-09-848-144-65	Sequence 65, Appl
288	9.8	54.4	42	9	US-10-027-806-86	Sequence 86, Appl	361	9.6	53.3	40	10	US-09-848-144-66	Sequence 66, Appl
289	9.8	54.4	42	9	US-09-835-659-9	Sequence 9, Appl1	362	9.6	53.3	43	10	US-09-027-287-40	Sequence 40, Appl
290	9.8	54.4	44	9	US-09-905-291A-21	Sequence 21, Appl	363	9.6	53.3	43	10	US-09-027-287-40	Sequence 40, Appl
291	9.8	54.4	44	10	US-09-909-088B-21	Sequence 21, Appl	364	9.6	53.3	44	10	US-09-875-519A-14	Sequence 14, Appl
292	9.8	54.4	44	10	US-09-909-088B-21	Sequence 21, Appl	365	9.6	53.3	44	10	US-09-875-519A-14	Sequence 14, Appl
293	9.8	54.4	48	10	US-09-735-995-100	Sequence 100, App	366	9.6	53.3	47	9	US-09-853-526-335	Sequence 335, App
294	9.8	54.4	17	8	US-08-375-291C-11	Sequence 11, Appl	367	9.6	53.3	48	12	US-09-901-484A-335	Sequence 335, App
295	9.6	53.3	17	10	US-09-866-108-6268	Sequence 6268, Ap	368	9.6	53.3	50	10	US-09-863-086-25	Sequence 32, App
296	9.6	53.3	17	10	US-09-866-108-6269	Sequence 6269, Ap	369	9.6	53.3	50	10	US-09-863-086-25	Sequence 32, App
297	9.6	53.3	17	10	US-09-866-108-7141	Sequence 7141, Ap	370	9.6	53.3	50	10	US-09-863-086-25	Sequence 26, Appl
298	9.6	53.3	17	10	US-09-866-108-7142	Sequence 7142, Ap	371	9.6	53.3	50	10	US-09-863-086-27	Sequence 27, Appl
299	9.6	53.3	17	10	US-09-866-108-9237	Sequence 9237, Ap	372	9.6	52.2	16	10	US-09-863-086-28	Sequence 28, Appl
300	9.6	53.3	17	10	US-09-866-108-9238	Sequence 9238, Ap	373	9.4	52.2	16	10	US-09-891-517-99	Sequence 89, Appl
301	9.6	53.3	19	9	US-10-032-495-23	Sequence 23, Appl	374	9.4	52.2	17	9	US-09-992-598-449	Sequence 95, Appl
302	9.6	53.3	20	10	US-09-179-536B-7	Sequence 7, Appl1	375	9.4	52.2	17	10	US-09-866-108-8216	Sequence 2216, Ap
303	9.6	53.3	20	10	US-09-825-497-34	Sequence 34, Appl1	376	9.4	52.2	17	10	US-09-866-108-8217	Sequence 2217, Ap
304	9.6	53.3	20	10	US-09-796-416-7	Sequence 7, Appl1	377	9.4	52.2	17	10	US-09-866-108-8214	Sequence 9104, Ap
305	9.6	53.3	20	10	US-09-791-406-14	Sequence 14, Appl	378	9.4	52.2	17	10	US-09-866-108-8105	Sequence 9105, Ap
306	9.6	53.3	20	10	US-09-879-341-7	Sequence 7, Appl1	379	9.4	52.2	17	10	US-09-866-108-8106	Sequence 9106, Ap
307	9.6	53.3	21	9	US-09-992-598-455	Sequence 455, App	380	9.4	52.2	17	10	US-09-866-108-8107	Sequence 9107, Ap
308	9.6	53.3	21	10	US-09-765-081-337	Sequence 337, App	381	9.4	52.2	17	10	US-09-866-108-8108	Sequence 9108, Ap
309	9.6	53.3	21	10	US-09-989-723-455	Sequence 455, App	382	9.4	52.2	17	10	US-09-866-108-8109	Sequence 9109, Ap
310	9.6	53.3	21	10	US-09-989-723-455	Sequence 455, App	383	9.4	52.2	17	10	US-09-866-108-8110	Sequence 9110, Ap
311	9.6	53.3	21	10	US-09-989-723-455	Sequence 455, App	384	9.4	52.2	17	10	US-09-899-980A-30	Sequence 30, Appl

C 385	9.4	52.2	17	10	US-09-989-722-429	Sequence 429, App	458	9.4	52.2	49	9	US-09-944-403-89	Sequence 89, Appl
C 386	9.4	52.2	17	10	US-09-989-723-429	Sequence 429, App	459	9.4	52.2	49	9	US-09-944-896-69	Sequence 89, Appl
C 387	9.4	52.2	17	10	US-09-989-279-429	Sequence 429, App	460	9.4	52.2	49	9	US-09-944-896-69	Sequence 89, Appl
C 388	9.4	52.2	17	10	US-09-989-727-429	Sequence 429, App	461	9.4	52.2	49	10	US-09-179-5368-119	Sequence 119, App
C 389	9.4	52.2	17	10	US-09-989-731-429	Sequence 429, App	462	9.4	52.2	49	10	US-09-866-028-89	Sequence 89, Appl
C 390	9.4	52.2	17	10	US-09-989-732-429	Sequence 429, App	463	9.4	52.2	49	10	US-09-989-122-427	Sequence 427, App
C 391	9.4	52.2	17	10	US-09-991-073-429	Sequence 429, App	464	9.4	52.2	49	10	US-09-989-723-427	Sequence 427, App
C 392	9.4	52.2	17	10	US-09-990-442-429	Sequence 429, App	465	9.4	52.2	49	10	US-09-989-779-427	Sequence 427, App
C 393	9.4	52.2	17	10	US-09-991-163-429	Sequence 429, App	466	9.4	52.2	49	10	US-09-989-727-427	Sequence 427, App
C 394	9.4	52.2	17	10	US-09-993-604-429	Sequence 429, App	467	9.4	52.2	49	10	US-09-944-449-89	Sequence 89, Appl
C 395	9.4	52.2	17	10	US-09-990-456-429	Sequence 429, App	468	9.4	52.2	49	10	US-09-989-731-427	Sequence 427, App
C 396	9.4	52.2	17	10	US-09-989-721-429	Sequence 429, App	469	9.4	52.2	49	10	US-09-944-457-89	Sequence 89, Appl
C 397	9.4	52.2	18	10	US-09-918-1864-40	Sequence 40, Appl	470	9.4	52.2	49	10	US-09-989-732-427	Sequence 427, App
C 398	9.4	52.2	18	10	US-09-918-1864-80	Sequence 80, Appl	471	9.4	52.2	49	10	US-09-991-073-427	Sequence 427, App
C 399	9.4	52.2	20	10	US-09-755-325-12	Sequence 12, Appl	472	9.4	52.2	49	10	US-09-945-587-89	Sequence 89, Appl
C 400	9.4	52.2	20	10	US-09-073-881-6	Sequence 6, Appl	473	9.4	52.2	49	10	US-09-990-442-427	Sequence 427, App
C 401	9.4	52.2	20	10	US-09-854-883-231	Sequence 231, App	474	9.4	52.2	49	10	US-09-991-163-427	Sequence 427, App
C 402	9.4	52.2	20	10	US-09-752-639-74	Sequence 74, Appl	475	9.4	52.2	49	10	US-09-945-015-89	Sequence 89, Appl
C 403	9.4	52.2	20	10	US-09-731-4578-83	Sequence 83, Appl	476	9.4	52.2	49	10	US-09-944-396-89	Sequence 89, Appl
C 404	9.4	52.2	20	10	US-09-984-198-74	Sequence 74, Appl	477	9.4	52.2	49	10	US-09-944-097-89	Sequence 89, Appl
C 405	9.4	52.2	20	10	US-09-797-779-6	Sequence 6, Appl	478	9.4	52.2	49	10	US-09-993-604-427	Sequence 427, App
C 406	9.4	52.2	20	10	US-09-791-243-65	Sequence 65, Appl	479	9.4	52.2	49	10	US-09-990-456-427	Sequence 427, App
C 407	9.4	52.2	21	9	US-09-803-320A-13	Sequence 13, Appl	480	9.4	52.2	49	10	US-09-944-432-89	Sequence 427, App
C 408	9.4	52.2	21	10	US-09-765-081-177	Sequence 177, App	481	9.4	52.2	49	10	US-09-943-762-89	Sequence 89, Appl
C 409	9.4	52.2	21	10	US-09-765-081-264	Sequence 264, App	482	9.4	52.2	49	10	US-09-944-554-89	Sequence 89, Appl
C 410	9.4	52.2	21	12	US-10-024-944-1	Sequence 1, Appl	483	9.4	52.2	49	10	US-09-989-721-427	Sequence 427, App
C 411	9.4	52.2	21	12	US-10-024-944-3	Sequence 3, Appl	484	9.4	52.2	49	10	US-09-943-851A-89	Sequence 89, Appl
C 412	9.4	52.2	22	12	US-10-024-944-2	Sequence 2, Appl	485	9.4	52.2	50	10	US-09-954-166-6	Sequence 6, Appl
C 413	9.4	52.2	24	9	US-09-959-519-5	Sequence 5, Appl	486	9.2	51.1	15	10	US-09-504-231A-1010	Sequence 1010, Ap
C 414	9.4	52.2	24	10	US-09-885-441-45	Sequence 45, Appl	487	9.2	51.1	15	10	US-09-274-533D-1010	Sequence 1010, Ap
C 415	9.4	52.2	25	10	US-09-866-108-5153	Sequence 5153, Ap	488	9.2	51.1	17	10	US-09-866-108-6266	Sequence 6266, Ap
C 416	9.4	52.2	25	10	US-09-866-108-5154	Sequence 5154, Ap	489	9.2	51.1	17	10	US-09-866-108-6267	Sequence 6267, Ap
C 417	9.4	52.2	25	10	US-09-866-108-13996	Sequence 13996, A	490	9.2	51.1	17	10	US-09-866-108-9221	Sequence 9227, Ap
C 418	9.4	52.2	25	10	US-09-866-108-13997	Sequence 13997, A	491	9.2	51.1	17	10	US-09-866-108-9223	Sequence 9231, Ap
C 419	9.4	52.2	25	10	US-09-866-108-13998	Sequence 13998, A	492	9.2	51.1	17	10	US-09-827-998-628	Sequence 628, App
C 420	9.4	52.2	25	10	US-09-866-108-13999	Sequence 13999, A	493	9.2	51.1	17	10	US-09-827-998-629	Sequence 629, App
C 421	9.4	52.2	25	10	US-09-866-108-14000	Sequence 14000, A	494	9.2	51.1	17	10	US-09-827-998-630	Sequence 630, App
C 422	9.4	52.2	25	10	US-09-866-108-14001	Sequence 14001, A	495	9.2	51.1	17	10	US-09-827-998-631	Sequence 631, App
C 423	9.4	52.2	25	10	US-09-866-108-14002	Sequence 14002, A	496	9.2	51.1	19	10	US-09-805-177-4	Sequence 4, Appl
C 424	9.4	52.2	25	10	US-09-866-108-14003	Sequence 14003, A	497	9.2	51.1	19	10	US-09-985-675-13	Sequence 13, Appl
C 425	9.4	52.2	25	10	US-09-866-108-14004	Sequence 14004, A	498	9.2	51.1	20	8	US-08-375-291C-14	Sequence 14, Appl
C 426	9.4	52.2	25	10	US-09-866-108-14005	Sequence 14005, A	499	9.2	51.1	20	9	US-09-946-807-80	Sequence 90, Appl
C 427	9.4	52.2	25	10	US-09-866-108-14006	Sequence 14006, A	500	9.2	51.1	20	10	US-09-755-325-12	Sequence 12, App
C 428	9.4	52.2	25	10	US-09-866-108-14007	Sequence 14007, A	501	9.2	51.1	20	10	US-09-772-105-35	Sequence 35, Appl
C 429	9.4	52.2	25	10	US-09-866-108-14008	Sequence 14008, A	502	9.2	51.1	20	10	US-09-795-668-90	Sequence 90, Appl
C 430	9.4	52.2	25	10	US-09-866-108-14009	Sequence 14009, A	503	9.2	51.1	20	10	US-09-854-883-150	Sequence 150, App
C 431	9.4	52.2	25	10	US-09-866-108-14010	Sequence 14010, A	504	9.2	51.1	20	10	US-09-350-259-30	Sequence 30, Appl
C 432	9.4	52.2	25	10	US-09-784-911-18	Sequence 18, Appl	505	9.2	51.1	20	10	US-09-752-639-143	Sequence 143, App
C 433	9.4	52.2	26	12	US-10-154-801-7	Sequence 7, Appl	506	9.2	51.1	20	10	US-09-785-686-90	Sequence 90, Appl
C 434	9.4	52.2	26	12	US-10-154-801-12	Sequence 12, Appl	507	9.2	51.1	20	10	US-09-964-198-143	Sequence 143, App
C 435	9.4	52.2	27	10	US-09-738-396-38	Sequence 38, Appl	508	9.2	51.1	20	10	US-09-844-268-2	Sequence 2, Appl
C 436	9.4	52.2	29	9	US-10-125-086-6	Sequence 6, Appl	509	9.2	51.1	20	10	US-09-844-106-73	Sequence 73, Appl
C 437	9.4	52.2	29	10	US-09-729-674-250	Sequence 250, App	510	9.2	51.1	20	10	US-09-791-406-73	Sequence 73, Appl
C 438	9.4	52.2	29	12	US-10-024-944-10	Sequence 10, Appl	511	9.2	51.1	20	10	US-09-791-942-26	Sequence 26, Appl
C 439	9.4	52.2	30	12	US-10-024-944-11	Sequence 11, Appl	512	9.2	51.1	20	10	US-09-791-942-51	Sequence 51, Appl
C 440	9.4	52.2	31	9	US-09-886-136-25	Sequence 25, Appl	513	9.2	51.1	20	12	US-10-028-158-13	Sequence 13, Appl
C 441	9.4	52.2	31	9	US-09-886-150-25	Sequence 25, Appl	514	9.2	51.1	21	10	US-09-179-5368-50	Sequence 50, Appl
C 442	9.4	52.2	31	10	US-09-801-274-326	Sequence 326, App	515	9.2	51.1	21	10	US-09-073-881-60	Sequence 60, Appl
C 443	9.4	52.2	31	10	US-09-801-274-1333	Sequence 1333, Ap	516	9.2	51.1	21	10	US-09-753-143-60	Sequence 60, Appl
C 444	9.4	52.2	31	10	US-09-801-274-1482	Sequence 1482, Ap	517	9.2	51.1	22	9	US-09-994-068-8	Sequence 8, Appl
C 445	9.4	52.2	31	10	US-09-893-817-26	Sequence 26, Appl	518	9.2	51.1	22	9	US-09-988-113-36	Sequence 36, Appl
C 446	9.4	52.2	34	10	US-09-764-246-11	Sequence 11, Appl	519	9.2	51.1	22	10	US-09-899-980A-32	Sequence 32, Appl
C 447	9.4	52.2	36	10	US-09-504-231A-2740	Sequence 2740, Ap	520	9.2	51.1	22	10	US-09-776-874A-36	Sequence 36, Appl
C 448	9.4	52.2	36	10	US-09-274-553D-2740	Sequence 2740, Ap	521	9.2	51.1	25	10	US-09-866-108-11158	Sequence 11158, A
C 449	9.4	52.2	40	10	US-09-349-954A-14	Sequence 14, Appl	522	9.2	51.1	25	10	US-09-866-108-11159	Sequence 11159, A
C 450	9.4	52.2	40	10	US-09-907-007-14	Sequence 14, Appl	523	9.2	51.1	25	10	US-09-866-108-14119	Sequence 14119, A
C 451	9.4	52.2	41	12	US-10-024-944-7	Sequence 7, Appl	524	9.2	51.1	25	10	US-09-866-108-14131	Sequence 14131, A
C 452	9.4	52.2	41	12	US-10-024-944-8	Sequence 8, Appl	525	9.2	51.1	25	10	US-09-827-998-1443	Sequence 1443, Ap
C 453	9.4	52.2	42	10	US-09-795-006A-13	Sequence 13, Appl	526	9.2	51.1	25	10	US-09-827-998-1444	Sequence 1444, Ap
C 454	9.4	52.2	48	10	US-09-714-4	Sequence 4, Appl	527	9.2	51.1	25	10	US-09-827-998-1445	Sequence 1445, Ap
C 455	9.4	52.2	48	10	US-09-972-715-4	Sequence 4, Appl	528	9.2	51.1	25	10	US-09-827-998-1446	Sequence 1446, Ap
C 456	9.4	52.2	49	9	US-09-944-413-89	Sequence 89, Appl	529	9.2	51.1	25	10	US-09-827-998-1447	Sequence 1447, Ap
C 457	9.4	52.2	49	9	US-09-992-598-427	Sequence 427, App	530	9.2	51.1	25	10	US-09-827-998-1448	Sequence 1448, Ap

531	9.2	51.1	25	10	US-09-827-998-1449	Sequence 1449, Ap	C 604	9	50.0	17	10	US-09-866-108-9236	Sequence 9236, Ap
532	9.2	51.1	25	10	US-09-827-998-1450	Sequence 1450, Ap	C 605	9	50.0	17	10	US-09-866-108-10002	Sequence 10002, A
533	9.2	51.1	25	10	US-09-827-998-1451	Sequence 1451, Ap	C 606	9	50.0	17	10	US-09-866-108-10095	Sequence 10095, A
534	9.2	51.1	25	10	US-09-827-998-1452	Sequence 1452, Ap	C 607	9	50.0	18	9	US-09-944-413-44	Sequence 44, Appl
535	9.2	51.1	25	10	US-09-827-998-1453	Sequence 1453, Ap	C 608	9	50.0	18	9	US-09-944-403-44	Sequence 44, Appl
536	9.2	51.1	25	10	US-09-827-998-1454	Sequence 1454, Ap	C 609	9	50.0	18	9	US-09-944-896-44	Sequence 44, Appl
537	9.2	51.1	26	9	US-09-828-995B-47	Sequence 47, Appl	C 610	9	50.0	18	9	US-09-944-944-44	Sequence 44, Appl
538	9.2	51.1	27	10	US-09-179-536B-111	Sequence 111, Appl	C 611	9	50.0	18	10	US-09-866-028-44	Sequence 44, Appl
539	9.2	51.1	27	10	US-09-037-657-37	Sequence 37, Appl	C 612	9	50.0	18	10	US-09-944-449-44	Sequence 44, Appl
540	9.2	51.1	28	10	US-09-804-690-13	Sequence 13, Appl	C 613	9	50.0	18	10	US-09-944-457-44	Sequence 44, Appl
541	9.2	51.1	28	10	US-09-962-805-12	Sequence 12, Appl	C 614	9	50.0	18	10	US-09-945-587-44	Sequence 44, Appl
542	9.2	51.1	29	9	US-09-879-813-7	Sequence 7, Appl	C 615	9	50.0	18	10	US-09-945-015-44	Sequence 44, Appl
543	9.2	51.1	29	9	US-09-852-209A-35	Sequence 35, Appl	C 616	9	50.0	18	10	US-09-944-986-44	Sequence 44, Appl
544	9.2	51.1	29	10	US-09-799-994-7	Sequence 7, Appl	C 617	9	50.0	18	10	US-09-944-097-44	Sequence 44, Appl
545	9.2	51.1	28	10	US-10-041-020-12	Sequence 12, Appl	C 618	9	50.0	18	10	US-09-944-432-44	Sequence 44, Appl
546	9.2	51.1	28	10	US-09-962-055-39	Sequence 39, Appl	C 619	9	50.0	18	10	US-09-944-762-44	Sequence 44, Appl
547	9.2	51.1	30	10	US-09-939-119-14	Sequence 14, Appl	C 620	9	50.0	18	10	US-09-944-654-44	Sequence 44, Appl
548	9.2	51.1	30	12	US-10-023-529-39	Sequence 39, Appl	C 621	9	50.0	18	10	US-09-943-851A-44	Sequence 44, Appl
549	9.2	51.1	30	12	US-10-023-523-39	Sequence 39, Appl	C 622	9	50.0	19	9	US-10-032-495-12	Sequence 12, Appl
550	9.2	51.1	31	10	US-09-801-274-166	Sequence 166, Appl	C 623	9	50.0	19	9	US-10-032-495-27	Sequence 27, Appl
551	9.2	51.1	31	10	US-09-801-274-197	Sequence 197, Appl	C 624	9	50.0	19	9	US-09-784-199-6	Sequence 6, Appl
552	9.2	51.1	31	10	US-09-801-274-228	Sequence 228, Appl	C 625	9	50.0	19	10	US-09-969-373-3115	Sequence 3115, Ap
553	9.2	51.1	31	10	US-09-801-274-405	Sequence 405, Appl	C 626	9	50.0	19	10	US-09-969-373-3948	Sequence 3948, Ap
554	9.2	51.1	31	10	US-09-801-274-585	Sequence 585, Appl	C 627	9	50.0	19	10	US-10-024-944-70	Sequence 23, Appl
555	9.2	51.1	31	10	US-09-801-274-612	Sequence 612, Appl	C 628	9	50.0	19	12	US-08-887-505-34	Sequence 20, Appl
556	9.2	51.1	31	10	US-09-801-274-881	Sequence 881, Appl	C 629	9	50.0	20	8	US-10-017-910-13	Sequence 34, Appl
557	9.2	51.1	31	10	US-09-801-274-694	Sequence 894, Appl	C 630	9	50.0	20	9	US-09-963-875-47	Sequence 13, Appl
558	9.2	51.1	31	10	US-09-801-274-1308	Sequence 1308, Ap	C 631	9	50.0	20	9	US-09-852-669-106	Sequence 47, Appl
559	9.2	51.1	31	10	US-09-801-274-1698	Sequence 1698, Ap	C 632	9	50.0	20	10	US-09-802-722-18	Sequence 106, Appl
560	9.2	51.1	33	9	US-09-832-659-17	Sequence 17, Appl	C 633	9	50.0	21	10	US-09-940-240-11	Sequence 18, Appl
561	9.2	51.1	33	9	US-09-832-659-19	Sequence 19, Appl	C 634	9	50.0	21	10	US-09-755-325-11	Sequence 12, Appl
562	9.2	51.1	33	9	US-09-832-659-37	Sequence 37, Appl	C 635	9	50.0	21	10	US-09-763-081-299	Sequence 299, Appl
563	9.2	51.1	33	9	US-09-832-659-39	Sequence 39, Appl	C 636	9	50.0	21	10	US-09-934-695-54	Sequence 54, Appl
564	9.2	51.1	33	9	US-09-832-659-39	Sequence 39, Appl	C 637	9	50.0	22	10	US-09-934-695-66	Sequence 66, Appl
565	9.2	51.1	34	10	US-09-835-341-9	Sequence 9, Appl	C 638	9	50.0	22	10	US-09-934-695-66	Sequence 66, Appl
566	9.2	51.1	34	10	US-09-808-860-3	Sequence 18, Appl	C 639	9	50.0	22	10	US-09-954-586-18	Sequence 48, Appl
567	9.2	51.1	34	10	US-09-896-866B-18	Sequence 18, Appl	C 640	9	50.0	22	10	US-09-954-586-54	Sequence 54, Appl
568	9.2	51.1	36	10	US-09-903-983-43	Sequence 43, Appl	C 641	9	50.0	22	10	US-09-954-586-54	Sequence 54, Appl
569	9.2	51.1	36	10	US-09-855-722-31	Sequence 23, Appl	C 642	9	50.0	22	10	US-09-954-586-60	Sequence 60, Appl
570	9.2	51.1	37	10	US-09-995-593A-23	Sequence 3, Appl	C 643	9	50.0	22	10	US-09-954-586-66	Sequence 66, Appl
571	9.2	51.1	38	10	US-09-727-405-3	Sequence 206, Appl	C 644	9	50.0	22	12	US-10-040-217-6	Sequence 6, Appl
572	9.2	51.1	39	10	US-09-623-959-206	Sequence 9, Appl	C 645	9	50.0	23	9	US-09-144-886-16	Sequence 16, Appl
573	9.2	51.1	42	10	US-10-013-718-9	Sequence 18, Appl	C 646	9	50.0	23	9	US-09-144-886-18	Sequence 18, Appl
574	9.2	51.1	40	10	US-09-834-291-18	Sequence 22, Appl	C 647	9	50.0	23	9	US-09-252-150-49	Sequence 49, Appl
575	9.2	51.1	40	10	US-09-834-291-26	Sequence 7, Appl	C 648	9	50.0	23	9	US-09-978-295A-565	Sequence 565, Appl
576	9.2	51.1	42	10	US-09-245-487B-22	Sequence 44, Appl	C 649	9	50.0	23	10	US-09-978-697-565	Sequence 565, Appl
577	9.2	51.1	44	10	US-09-888-358-7	Sequence 2, Appl	C 650	9	50.0	23	10	US-09-878-262B-7	Sequence 7, Appl
578	9.2	51.1	44	10	US-09-905-983-44	Sequence 2, Appl	C 651	9	50.0	23	10	US-09-778-879A-23	Sequence 23, Appl
579	9.2	51.1	44	10	US-09-803-165-2	Sequence 148, App	C 652	9	50.0	23	10	US-09-778-880A-23	Sequence 20, Appl
580	9.2	51.1	46	10	US-09-263-959-128	Sequence 418, App	C 653	9	50.0	23	10	US-09-988-899-70	Sequence 12, Appl
581	9.2	51.1	47	9	US-09-978-295A-418	Sequence 364, App	C 654	9	50.0	23	10	US-09-988-899-70	Sequence 6, Appl
582	9.2	51.1	47	9	US-09-905-291A-364	Sequence 364, App	C 655	9	50.0	23	10	US-10-036-283A-12	Sequence 33, Appl
583	9.2	51.1	47	9	US-09-978-697-418	Sequence 148, App	C 656	9	50.0	23	12	US-10-036-283A-12	Sequence 26, Appl
584	9.2	51.1	49	9	US-09-978-697-418	Sequence 148, App	C 657	9	50.0	24	9	US-09-992-598-141	Sequence 141, App
585	9.2	51.1	49	9	US-09-978-697-418	Sequence 148, App	C 658	9	50.0	24	10	US-09-989-723-141	Sequence 141, App
586	9.2	51.1	50	10	US-09-978-697-418	Sequence 148, App	C 659	9	50.0	24	10	US-09-989-723-141	Sequence 141, App
587	9.2	51.1	50	10	US-09-978-697-418	Sequence 148, App	C 660	9	50.0	24	10	US-09-989-723-141	Sequence 141, App
588	9.2	51.1	50	10	US-09-978-697-418	Sequence 148, App	C 661	9	50.0	24	10	US-09-989-723-141	Sequence 141, App
589	9.2	51.1	50	10	US-09-978-697-418	Sequence 148, App	C 662	9	50.0	24	10	US-09-989-723-141	Sequence 141, App
590	9.2	51.1	50	10	US-09-978-697-418	Sequence 148, App	C 663	9	50.0	24	10	US-09-989-723-141	Sequence 141, App
591	9.2	51.1	50	10	US-09-978-697-418	Sequence 148, App	C 664	9	50.0	24	10	US-09-989-723-141	Sequence 141, App
592	9.2	51.1	50	10	US-09-978-697-418	Sequence 148, App	C 665	9	50.0	24	10	US-09-989-723-141	Sequence 141, App
593	9.2	51.1	50	10	US-09-978-697-418	Sequence 148, App	C 666	9	50.0	24	10	US-09-989-723-141	Sequence 141, App
594	9.2	51.1	50	10	US-09-978-697-418	Sequence 148, App	C 667	9	50.0	24	10	US-09-989-723-141	Sequence 141, App
595	9.2	51.1	50	10	US-09-978-697-418	Sequence 148, App	C 668	9	50.0	24	10	US-09-989-723-141	Sequence 141, App
596	9.2	51.1	50	10	US-09-978-697-418	Sequence 148, App	C 669	9	50.0	24	10	US-09-989-723-141	Sequence 141, App
597	9.2	51.1	50	10	US-09-978-697-418	Sequence 148, App	C 670	9	50.0	24	10	US-09-989-723-141	Sequence 141, App
598	9.2	51.1	50	10	US-09-978-697-418	Sequence 148, App	C 671	9	50.0	24	10	US-09-989-723-141	Sequence 141, App
599	9.2	51.1	50	10	US-09-978-697-418	Sequence 148, App	C 672	9	50.0	24	10	US-09-989-723-141	Sequence 141, App
600	9.2	51.1	50	10	US-09-978-697-418	Sequence 148, App	C 673	9	50.0	24	10	US-09-989-723-141	Sequence 141, App
601	9.2	51.1	50	10	US-09-978-697-418	Sequence 148, App	C 674	9	50.0	24	10	US-09-989-723-141	Sequence 141, App
602	9.2	51.1	50	10	US-09-978-697-418	Sequence 148, App	C 675	9	50.0	24	10	US-09-989-723-141	Sequence 141, App
603	9.2	51.1	50	10	US-09-978-697-418	Sequence 148, App	C 676	9	50.0	24	10	US-09-989-723-141	Sequence 141, App

677	9	50.0	25	10	US-09-866-108-4245	Sequence 4245, Ap	C 750	9	50.0	31	9	US-09-736-968A-111	Sequence 111, App
678	9	50.0	25	10	US-09-866-108-4246	Sequence 4246, Ap	751	9	50.0	31	10	US-09-801-774-409	Sequence 409, App
679	9	50.0	25	10	US-09-866-108-4247	Sequence 4247, Ap	752	9	50.0	32	10	US-09-318-271-13	Sequence 13, App1
680	9	50.0	25	10	US-09-866-108-4248	Sequence 4248, Ap	753	9	50.0	32	10	US-09-745-605-21	Sequence 21, App1
681	9	50.0	25	10	US-09-866-108-4249	Sequence 4249, Ap	754	9	50.0	33	9	US-09-939-883-3	Sequence 3, App1
682	9	50.0	25	10	US-09-866-108-4250	Sequence 4250, Ap	C 755	9	50.0	33	10	US-09-939-754-3	Sequence 3, App1
683	9	50.0	25	10	US-09-866-108-4251	Sequence 4251, Ap	756	9	50.0	33	10	US-09-745-605-35	Sequence 35, App1
684	9	50.0	25	10	US-09-866-108-4252	Sequence 4252, Ap	C 757	9	50.0	33	10	US-09-939-802-10	Sequence 10, App1
685	9	50.0	25	10	US-09-866-108-4253	Sequence 4253, Ap	758	9	50.0	34	9	US-09-987-107-85	Sequence 85, App1
686	9	50.0	25	10	US-09-866-108-4254	Sequence 4254, Ap	C 759	9	50.0	35	9	US-09-974-052-40	Sequence 40, App1
687	9	50.0	25	10	US-09-866-108-4255	Sequence 4255, Ap	C 760	9	50.0	35	9	US-09-453-289-1	Sequence 1, App1
688	9	50.0	25	10	US-09-866-108-4256	Sequence 4256, Ap	C 761	9	50.0	35	10	US-09-826-212-21	Sequence 21, App1
689	9	50.0	25	10	US-09-866-108-4257	Sequence 4257, Ap	C 762	9	50.0	35	10	US-09-826-212-25	Sequence 25, App1
690	9	50.0	25	10	US-09-866-108-4258	Sequence 4258, Ap	C 763	9	50.0	35	10	US-09-214-606-1	Sequence 1, App1
691	9	50.0	25	10	US-09-866-108-4259	Sequence 4259, Ap	C 764	9	50.0	35	10	US-09-861-992-29	Sequence 29, App1
C 692	9	50.0	25	10	US-09-866-108-5235	Sequence 5235, Ap	C 765	9	50.0	35	12	US-10-036-507-16	Sequence 16, App1
C 693	9	50.0	25	10	US-09-866-108-5236	Sequence 5236, Ap	C 766	9	50.0	36	9	US-09-974-052-41	Sequence 41, App1
C 694	9	50.0	25	10	US-09-866-108-5237	Sequence 5237, Ap	767	9	50.0	36	10	US-09-006-298-2	Sequence 2, App1
C 695	9	50.0	25	10	US-09-866-108-5238	Sequence 5238, Ap	C 768	9	50.0	36	10	US-09-854-799-4	Sequence 4, App1
C 696	9	50.0	25	10	US-09-866-108-5239	Sequence 5239, Ap	769	9	50.0	36	10	US-09-375-924C-9	Sequence 9, App1
C 697	9	50.0	25	10	US-09-866-108-5240	Sequence 5240, Ap	C 770	9	50.0	38	10	US-09-746-359A-48	Sequence 48, App1
C 698	9	50.0	25	10	US-09-866-108-5241	Sequence 5241, Ap	C 771	9	50.0	38	10	US-09-987-456-34	Sequence 34, App1
C 699	9	50.0	25	10	US-09-866-108-5242	Sequence 5242, Ap	772	9	50.0	39	10	US-09-987-456-63	Sequence 63, App1
C 700	9	50.0	25	10	US-09-866-108-5243	Sequence 5243, Ap	C 773	9	50.0	40	10	US-09-790-417-181	Sequence 181, App
C 701	9	50.0	25	10	US-09-866-108-11170	Sequence 11170, A	774	9	50.0	40	10	US-09-245-802-26	Sequence 26, App
C 702	9	50.0	25	10	US-09-866-108-12161	Sequence 12161, A	C 775	9	50.0	40	10	US-09-245-802-94	Sequence 94, App1
C 703	9	50.0	25	10	US-09-866-108-12178	Sequence 12178, A	C 776	9	50.0	40	10	US-09-245-802-120	Sequence 120, App
C 704	9	50.0	25	10	US-09-866-108-13122	Sequence 13122, A	C 777	9	50.0	41	10	US-09-358-082A-12	Sequence 12, App1
C 705	9	50.0	25	10	US-09-866-108-13123	Sequence 13123, A	C 778	9	50.0	41	10	US-09-861-292-25	Sequence 25, App1
C 706	9	50.0	25	10	US-09-866-108-13124	Sequence 13124, A	C 779	9	50.0	45	9	US-09-905-221A-146	Sequence 146, App
C 707	9	50.0	25	10	US-09-866-108-13125	Sequence 13125, A	C 780	9	50.0	45	10	US-09-909-320-146	Sequence 146, App
C 708	9	50.0	25	10	US-09-866-108-13126	Sequence 13126, A	C 781	9	50.0	45	10	US-09-909-088B-146	Sequence 146, App
C 709	9	50.0	25	10	US-09-866-108-13127	Sequence 13127, A	C 782	9	50.0	48	9	US-09-944-413-115	Sequence 115, App
C 710	9	50.0	25	10	US-09-866-108-13128	Sequence 13128, A	783	9	50.0	48	9	US-09-944-403-115	Sequence 115, App
C 711	9	50.0	25	10	US-09-866-108-13129	Sequence 13129, A	C 784	9	50.0	48	9	US-09-944-896-115	Sequence 115, App
C 712	9	50.0	25	10	US-09-866-108-13130	Sequence 13130, A	C 785	9	50.0	48	9	US-09-944-944-115	Sequence 115, App
C 713	9	50.0	25	10	US-09-866-108-14128	Sequence 14128, A	786	9	50.0	48	10	US-09-753-436-67	Sequence 67, App1
C 714	9	50.0	25	10	US-09-866-108-14884	Sequence 14884, A	C 787	9	50.0	48	10	US-09-866-028-115	Sequence 115, App
C 715	9	50.0	25	10	US-09-866-108-14885	Sequence 14885, A	788	9	50.0	48	10	US-09-944-449-115	Sequence 115, App
C 716	9	50.0	25	10	US-09-866-108-14886	Sequence 14886, A	789	9	50.0	48	10	US-09-944-457-115	Sequence 115, App
C 717	9	50.0	25	10	US-09-866-108-14887	Sequence 14887, A	C 790	9	50.0	48	10	US-09-944-587-115	Sequence 115, App
C 718	9	50.0	25	10	US-09-866-108-14888	Sequence 14888, A	791	9	50.0	48	10	US-09-945-015-115	Sequence 115, App
C 719	9	50.0	25	10	US-09-866-108-14889	Sequence 14889, A	C 792	9	50.0	48	10	US-09-945-015-115	Sequence 115, App
C 720	9	50.0	25	10	US-09-866-108-14900	Sequence 14900, A	793	9	50.0	48	10	US-09-944-396-115	Sequence 115, App
C 721	9	50.0	25	10	US-09-866-108-14901	Sequence 14901, A	C 794	9	50.0	48	10	US-09-944-332-115	Sequence 115, App
C 722	9	50.0	25	10	US-09-866-108-14902	Sequence 14902, A	795	9	50.0	48	10	US-09-943-762-115	Sequence 115, App
C 723	9	50.0	25	10	US-09-866-108-14987	Sequence 14987, A	796	9	50.0	48	10	US-09-944-654-115	Sequence 115, App
C 724	9	50.0	25	10	US-09-866-108-14988	Sequence 14988, A	C 797	9	50.0	48	10	US-09-943-851A-115	Sequence 115, App
C 725	9	50.0	25	10	US-09-866-108-14989	Sequence 14989, A	798	9	50.0	50	10	US-09-999-672-22	Sequence 22, App1
C 726	9	50.0	25	10	US-09-866-108-14990	Sequence 14990, A	C 799	9	50.0	50	12	US-10-040-863-22	Sequence 22, App1
C 727	9	50.0	25	10	US-09-866-108-14991	Sequence 14991, A	C 800	9	50.0	50	10	US-09-751-261-9	Sequence 9, App1
C 728	9	50.0	25	10	US-09-866-108-14992	Sequence 14992, A	C 801	8.8	48.9	15	10	US-09-811-286-14	Sequence 14, App1
C 729	9	50.0	25	10	US-09-866-108-14993	Sequence 14993, A	C 802	8.8	48.9	15	10	US-09-504-231A-243	Sequence 243, App
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ALIGNMENTS

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RESULT 1
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; Sequence 22, Application US/09761116
; Patent No. US20020102552A1
; GENERAL INFORMATION:
; APPLICANT: American Home Products Corp.
; APPLICANT: Susulic, Vedrana S.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION OF THE HUMAN
; FILE REFERENCE: 0630/0E791
; CURRENT APPLICATION NUMBER: US/09/761,116
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 09/243,335
; PRIOR FILING DATE: 1999-02-01
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
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; TYPE: DNA
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; FEATURE:
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US-09-761-116-22
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RESULT 2
US-09-252-150-51
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; Sequence 51, Application US/09252150A
; Patent No. US20020155604A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden Ledbetter, Martha
; APPLICANT: Brady, William A.
; APPLICANT: Grosmaire, Laura S.
; APPLICANT: Law, Che-Leung
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING
; FILE REFERENCE: 9113-0019-999
; CURRENT APPLICATION NUMBER: US/09/252,150A
; CURRENT FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: US 60/075,274
; EARLIER FILING DATE: 1998-02-19
; EARLIER APPLICATION NUMBER: US 60/108,683
; EARLIER FILING DATE: 1998-11-16
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 3.0
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US-09-252-150-51
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RESULT 3
US-09-866-108-1470
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; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOmica-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 1470
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-1470

Query Match      65.6%; Score 11.8; DB 10; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4  GGAGGCGAGCTGCGC 18
        ||||| |||||
DB      3  GGAGGCGAGCGCTGCC 17

RESULT 4
US-09-866-108-1471
; Sequence 1471, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
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; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 1471
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-1471

Query Match      65.6%; Score 11.8; DB 10; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4  GGAGGCGAGCTGCGC 18
        ||||| |||||
DB      2  GGAGGCGAGCGCTGCC 16

RESULT 5
US-09-866-108-1472
; Sequence 1472, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 1472
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-1472

Query Match      65.6%; Score 11.8; DB 10; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.2e+03;
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Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 GGAAGCAGCTGGC 18
|||||
Db 1 GGAAGGAGGCTGGC 15

RESULT 6
US-09-866-108-4399
; Sequence 4399, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 4399
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-4399

Query Match 65.6%; Score 11.8; DB 10; Length 25;
Best Local Similarity 86.7%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 GGAAGCAGCTGGC 18
|||||
Db 11 GGAAGGAGGCTGGC 25

RESULT 7
US-09-866-108-4400
; Sequence 4400, Application US/09866108

; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 4400
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-4400

Query Match 65.6%; Score 11.8; DB 10; Length 25;
Best Local Similarity 86.7%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 GGAAGCAGCTGGC 18
|||||
Db 10 GGAAGGAGGCTGGC 24

RESULT 8
US-09-866-108-4401
; Sequence 4401, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE


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FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 60/266,860
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aecomica Sequence Listing Engine
SEQ ID NO 4401
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-4401

Query Match      65.6%; Score 11.8; DB 10; Length 25;
Best Local Similarity 86.7%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4  GGAGGCGAGCTGGC 18
        ||||| 11 |||||
DB      9  GGAGGCGAGCTGGC 23

RESULT 9
US-09-866-108-4402
Sequence 4402, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aecomica Sequence Listing Engine
SEQ ID NO 4402
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-4402

Query Match      65.6%; Score 11.8; DB 10; Length 25;
Best Local Similarity 86.7%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4  GGAGGCGAGCTGGC 18
        ||||| 11 |||||
DB      8  GGAGGCGAGCTGGC 22

RESULT 10
US-09-866-108-4403
Sequence 4403, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
```

```
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 4403
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-4403
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```
Query Match 65.6%; Score 11.8; DB 10; Length 25;
Best Local Similarity 86.7%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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OY 4 GGAAGCAGCTGGC 18
    ||||| |||||
DB 7 GGAAGGAGGCTGGC 21
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RESULT 11

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US-09-866-108-4404
; Sequence 4404, Application US/09866108
; Patent No. US2002004800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 4405
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-4405
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; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 4404
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-4404
```

```
Query Match 65.6%; Score 11.8; DB 10; Length 25;
Best Local Similarity 86.7%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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OY 4 GGAAGCAGCTGGC 18
    ||||| |||||
DB 6 GGAAGGAGGCTGGC 20
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RESULT 12

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US-09-866-108-4405
; Sequence 4405, Application US/09866108
; Patent No. US2002004800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 4405
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-4405
```

Query Match 65.6%; Score 11.8; DB 10; Length 25;
Best Local Similarity 86.7%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 GGAAGCAGCTCGGC 18
| | | | | | | | | |
Db 5 GGAAGGAGAGCTGCG 19

RESULT 13

US-09-866-108-4406
; Sequence 4406, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 4406
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-4406

Query Match 65.6%; Score 11.8; DB 10; Length 25;
Best Local Similarity 86.7%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 GGAAGCAGCTCGGC 18
| | | | | | | | | |
Db 4 GGAAGGAGAGCTGCG 18

RESULT 14

US-09-866-108-4407
; Sequence 4407, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David R.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 4407
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-4407

Query Match 65.6%; Score 11.8; DB 10; Length 25;
Best Local Similarity 86.7%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 GGAAGCAGCTCGGC 18
| | | | | | | | | |
Db 3 GGAAGGAGAGCTGCG 17

RESULT 15

US-09-866-108-4408
; Sequence 4408, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.

```
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 4408
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-4408

Query Match      65.6%; Score 11.8; DB 10; Length 25;
Best Local Similarity 86.7%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 4 GGAAGCAGCTCTGCG 18
    ||||| |||||
Db 2 GGAAGGAGAGCTGCG 16

RESULT 16
US-09-866-108-4409
; Sequence 4409, Application US/09866108
; Patent No. US2002004800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
```

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; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 4409
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-4409

Query Match      65.6%; Score 11.8; DB 10; Length 25;
Best Local Similarity 86.7%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 4 GGAAGCAGCTCTGCG 18
    ||||| |||||
Db 1 GGAAGGAGAGCTGCG 15

RESULT 17
US-09-263-959-758/C
; Sequence 758, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: KOOP, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH U
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
```

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 758:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-758

Query Match          65.6%; Score 11.8; DB 10; Length 40;
Best Local Similarity 86.7%; Pred. No. 2.3e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGAAGCAGCTCTGGC 18
    |||||
DB 39 GGAAGCAGCAGCGGC 25

RESULT 18
US-10-032-495-31/c
; Sequence 31, Application US/10032495
; Patent No. US20020155601A1
; GENERAL INFORMATION:
; APPLICANT: YAN, MEN LIANG
; TITLE OF INVENTION: METHOD FOR PRODUCING A POPULATION OF HOMOZYGOUS STEM
; TITLE OF INVENTION: CELLS HAVING A PRE-SELECTED IMMUNOTYPE AND/OR GENOTYPE,
; TITLE OF INVENTION: MATERIALS AND METHODS USING SAME
; FILE REFERENCE: 0249-0002US
; CURRENT APPLICATION NUMBER: US/10/032,495
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: 60/258,881
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
US-10-032-495-31

Query Match          64.4%; Score 11.6; DB 9; Length 19;
Best Local Similarity 77.8%; Pred. No. 2.8e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCCGAGAGCAGCTCTGGC 18
    |||||
DB 19 CCTGGAGACAGCGCGGC 2

RESULT 19
US-09-769-207A-15
; Sequence 15, Application US/09769207A
; Patent No. US20020132234A1
; GENERAL INFORMATION:
; APPLICANT: DZGenes, LLC
; TITLE OF INVENTION: NITRIC OXIDE SYNTHASE GENE DIAGNOSTIC POLYMORPHISMS
; FILE REFERENCE: DZG 2165.1
; CURRENT APPLICATION NUMBER: US/09/769,207A
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: US 60/117,775
; PRIOR FILING DATE: 2000-01-24
; PRIOR APPLICATION NUMBER: US 60/220,662
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 22
; TYPE: DNA
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```

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Misc_feature
; LOCATION: (1)-(22)
; OTHER INFORMATION: STAT_1 (Se-Cys tRNA gene transcription activating factor)
US-09-769-207A-15

Query Match          64.4%; Score 11.6; DB 10; Length 22;
Best Local Similarity 77.8%; Pred. No. 2.8e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCCGAGAGCAGCTCTGGC 18
    |||||
DB 5 CCCAGCATGCACCTCTGGC 22

RESULT 20
US-09-801-274-826
; Sequence 826, Application US/09801274
; Patent No. US20020032319A1
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825.2009-001
; CURRENT APPLICATION NUMBER: US/09/801,274
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/187,510
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 60/206,129
; NUMBER OF SEQ ID NOS: 1802
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 826
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-274-826

Query Match          64.4%; Score 11.6; DB 10; Length 31;
Best Local Similarity 77.8%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCCGAGAGCAGCTCTGGC 18
    |||||
DB 12 CCTTAAAGCGCGGCTGGC 29

RESULT 21
US-09-780-669-942/c
; Sequence 942, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
```

```
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 942
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-942

Query Match
Best Local Similarity 64.4%; Score 11.6; DB 10; Length 45;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CCGGAGGCGAGCTGGC 18
Db 30 CACGCTAGGCAATTCGCC 13

RESULT 22
US-09-822-827-942/C
; Sequence 942, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 942
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-942

Query Match
Best Local Similarity 64.4%; Score 11.6; DB 10; Length 45;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CCGGAGGCGAGCTGGC 18
Db 30 CACGCTAGGCAATTCGCC 13

RESULT 23
US-09-825-414-81/C
; Sequence 81, Application US/09825414
; Patent No. US20020083489A1
; GENERAL INFORMATION:
; APPLICANT: Collier, Alan
; APPLICANT: Alfano, James R.
; APPLICANT: Charkowski, Amy O.
; TITLE OF INVENTION: DNA MOLECULES AND POLYPEPTIDES OF PSEUDOMONAS SYRINGAE
; TITLE OF INVENTION: HRP PATHOGENICITY ISLAND AND THEIR USES
; FILE REFERENCE: 19603/3243
; CURRENT APPLICATION NUMBER: US/09/825,414
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/194,160
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: 60/224,604
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/249,548
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
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; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-825-414-81

Query Match
Best Local Similarity 63.3%; Score 11.4; DB 10; Length 28;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 CCGGAGGCGAGTC 14
Db 26 CTGGAAGCGAGTC 14

RESULT 24
US-09-870-203A-25
; Sequence 25, Application US/09870203A
; Patent No. US20020137213A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020137213A1art1s AG
; TITLE OF INVENTION: Adenovirus particles with mutagenized fiber proteins
; FILE REFERENCE: 4-31452A
; CURRENT APPLICATION NUMBER: US/09/870,203A
; CURRENT FILING DATE: 2001-05-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
; NAME/KEY: primer_bind
; LOCATION: (1)..(36)
; OTHER INFORMATION:
US-09-870-203A-25

Query Match
Best Local Similarity 63.3%; Score 11.4; DB 10; Length 36;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 AAGCGAGCTGGC 18
Db 20 AAGCGAGCTGGC 32

RESULT 25
US-09-870-203A-26/C
; Sequence 26, Application US/09870203A
; Patent No. US20020137213A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020137213A1art1s AG
; TITLE OF INVENTION: Adenovirus particles with mutagenized fiber proteins
; FILE REFERENCE: 4-31452A
; CURRENT APPLICATION NUMBER: US/09/870,203A
; CURRENT FILING DATE: 2001-05-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
; NAME/KEY: primer_bind
; LOCATION: (1)..(36)
; OTHER INFORMATION:
US-09-870-203A-26

Query Match
Best Local Similarity 63.3%; Score 11.4; DB 10; Length 36;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Matches 12: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AAGCAGCTGTGGC 18
| | | | | | | | | |
Db 17 AAGCAGCTGTGGC 5

RESULT 26

US-09-853-386-151/C
; Sequence 151, Application US/09853386
; Patent No. US20020049151A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Evelyn
; APPLICANT: Bresnahan, Barry
; APPLICANT: Conneely, Orla
; APPLICANT: Fitzgerald, Oliver
; TITLE OF INVENTION: Therapeutic Approaches to Diseases by Suppression of the NMR
; FILE REFERENCE: P01972051
; CURRENT APPLICATION NUMBER: US/09/853,386
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/203645
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 151
; LENGTH: 20
; TYPE: DNA
; ORGANISM: HUMAN
US-09-853-386-151

Query Match 62.2%; Score 11.2; DB 10; Length 20;
Best Local Similarity 81.2%; Pred. No. 4.5e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CCGAAGCAGCTGTG 17
| | | | | | | | | |
Db 16 CAGGAAGCAGCTGAG 1

RESULT 27

US-09-765-081-41/C
; Sequence 41, Application US/09765081
; Patent No. US20020037508A1
; GENERAL INFORMATION:
; APPLICANT: Carrigill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825.2008-001
; CURRENT APPLICATION NUMBER: US/09/765,081
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,861
; PRIOR FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-765-081-41

Query Match 62.2%; Score 11.2; DB 10; Length 21;
Best Local Similarity 72.2%; Pred. No. 4.5e+03;
Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCGGAAGCAGCTGTGGC 18
| | | | | | | | | |
Db 21 CCTGATATATGTCTGGC 4

RESULT 28
US-09-846-573B-7/c

; Sequence 7, Application US/09846573B
; Patent No. US20020077467A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Moore, Emma E.
; APPLICANT: Raymond, Fenella
; TITLE OF INVENTION: Mammalian Calcitonin-like Polypeptide-1
; FILE REFERENCE: 97-73C1
; CURRENT APPLICATION NUMBER: US/09/846,573B
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/213,634
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/069,976
; PRIOR FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-846-573B-7

Query Match 62.2%; Score 11.2; DB 10; Length 21;
Best Local Similarity 81.2%; Pred. No. 4.5e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CCGAAGCAGCTGTG 17
| | | | | | | | | |
Db 19 CCGAAGCAGCTGTGG 4

RESULT 29
US-09-235-594-7/c
; Sequence 7, Application US/09235594
; Patent No. US20010014659A1
; GENERAL INFORMATION:
; APPLICANT: Convents, Andre C.
; APPLICANT: Moese, Rosa Laura
; TITLE OF INVENTION: LAUNDRY AND CLEANING COMPOSITIONS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE PROCTER & GAMBLE COMPANY
; STREET: 11810 East Miami River Road
; CITY: Ross
; STATE: OH
; COUNTRY: USA
; ZIP: 45061

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/235,594
; FILING DATE: January 22, 1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cook, C. Brant
; REGISTRATION NUMBER: 39,151
; REFERENCE/DOCKET NUMBER: 6613
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (513) 627-0032
; TELEFAX: (513) 627-0318
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-235-594-7

Query Match	62.2%;	Score 11.2;	DB 10;	Length 28;
Best Local Similarity	81.2%;	Pred. No. 4.6e+03;		
Matches 13; Conservative	0;	Mismatches 3;	Indels	

QY	3	CGAAGGCAGTCTGGC	18
Db	16	CGAAGCCAGGGTGGC	1

RESULT 30

US-09-765-780A-10/c
; Sequence 10, Application US/09765780A

; GENERAL INFORMATION:

Inglis, Stephen C.

Immunogens, and Vaccines

CORRESPONDENCE ADDRESS:

STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco

STATE: CA
COUNTRY: USA

ZIP: 94111-4187
COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
MEDIUM TYPE: floppy disk

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

APPLICATION NUMBER: US/09/765,780A

PRIOR APPLICATION DATA:

FILING DATE: 1996-02-21

FILING DATE: 28-JUL-1995

FILING DATE: 16-FEB-1996

NAME: Linda R. Judge
REGISTRATION NUMBER:

TELECOMMUNICATION INFORMATION

TELEPHONE: (415) 871-1111
TELEFAX: (415) 949-8888

SEQUENCE CHARACTERISTICS

TYPE: nucleic acid

TOPOLOGY: 1

ANTI-SENSE: NO

US-09-765-780A-10

Query Match
Post 100% Simil

Matches 13; Conservative 0; M

CCCGGAGGCAGTCT

DD 1 / CCGGAACTGATTCG 2

RESULT 31

; Sequence 10, Application US/09765870

GENERAL INFORMATION:


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: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/727,311
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/767,436
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn A
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P31 9072
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-9001
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 25:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 36 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
US-09-727-311-25
:
Query Match          62.2%; Score 11.2; DB 10; Length 36;
Best Local Similarity 81.2%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCGGAGCGAGCTCTGG 17
DB 12 CCGGATGGAAATTCGTG 27

RESULT 33
US-09-727-311-36
: Sequence 36, Application US/09727311
: Patent No. US20010024782A1
: GENERAL INFORMATION:
: APPLICANT: Huse, William D.
: TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
: TITLE OF INVENTION: RANDOMIZED PEPTIDES
: NUMBER OF SEQUENCES: 61
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
: STREET: 444 South Flower Street, Suite 2000
: CITY: Los Angeles
: STATE: California
: COUNTRY: United States
: ZIP: 90071
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/727,311
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/767,436
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn A
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P31 9072
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-9001
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 36:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 36 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
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: TOPOLOGY: linear
:
US-09-727-311-36
:
Query Match          62.2%; Score 11.2; DB 10; Length 36;
Best Local Similarity 81.2%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCGGAGCGAGCTCTGG 17
DB 12 CCGGATGGAAATTCGTG 27

RESULT 34
US-09-870-203A-29
: Sequence 29, Application US/09870203A
: Patent No. US20020137213A1
: GENERAL INFORMATION:
: APPLICANT: NO. US20020137213A1artis AG
: TITLE OF INVENTION: Adenovirus particles with mutagenized fiber proteins
: FILE REFERENCE: 4-31452A
: CURRENT APPLICATION NUMBER: US/09/870,203A
: CURRENT FILING DATE: 2001-05-30
: NUMBER OF SEQ ID NOS: 43
: SOFTWARE: Patentin version 3.1
: SEQ ID NO: 29
: LENGTH: 36
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: NAME/KEY: primer_bind
: LOCATION: (1)..(36)
: OTHER INFORMATION:
:
US-09-870-203A-29
:
Query Match          62.2%; Score 11.2; DB 10; Length 36;
Best Local Similarity 81.2%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CCGAGCGAGCTCTGGC 18
DB 17 CTGCGAGCGAGTTTGGC 32

RESULT 35
US-09-870-203A-30/C
: Sequence 30, Application US/09870203A
: Patent No. US20020137213A1
: GENERAL INFORMATION:
: APPLICANT: NO. US20020137213A1artis AG
: TITLE OF INVENTION: Adenovirus particles with mutagenized fiber proteins
: FILE REFERENCE: 4-31452A
: CURRENT APPLICATION NUMBER: US/09/870,203A
: CURRENT FILING DATE: 2001-05-30
: NUMBER OF SEQ ID NOS: 43
: SOFTWARE: Patentin version 3.1
: SEQ ID NO: 30
: LENGTH: 36
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: NAME/KEY: primer_bind
: LOCATION: (1)..(36)
: OTHER INFORMATION:
:
US-09-870-203A-30
:
Query Match          62.2%; Score 11.2; DB 10; Length 36;
Best Local Similarity 81.2%; Pred. No. 4.7e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CCGAGCGAGCTCTGGC 18
DB 17 CTGCGAGCGAGTTTGGC 32
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Db          20 CTGCAGCGCGATTGGC 5

RESULT 36
US-09-908-599-19/c
; Sequence 19, Application US/09908599
; Patent No. US20020055147A1
; GENERAL INFORMATION:
; APPLICANT: Li, Haodong et al.
; TITLE OR INVENTION: Human Chemokine Beta 13
; FILE REFERENCE: PRI177P3
; CURRENT APPLICATION NUMBER: US/09/908,599
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/432,768
; PRIOR FILING DATE: 1999-11-03
; PRIOR APPLICATION NUMBER: 60/032,432
; PRIOR FILING DATE: 1996-12-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-599-19

```

Query	Score	DB	Length
62.2%	11.2	10	46
Best Local Similarity	81.2%		
Matches	13	Conservative	0
		Mismatches	3
		Indels	0
		Gaps	0

```

RESULT 37
US-09-908-599-21/c
: Sequence 21, Application US/09080599
: Patent No. US20020055147A1
:
: GENERAL INFORMATION:
:
: APPLICANT: Li, Haodong et al.
:
: TITLE OF INVENTION: Human Chemokine Beta 13
: FILE REFERENCE: PE177P3
:
: CURRENT APPLICATION NUMBER: US/09/908,599
: CURRENT FILING DATE: 2001-07-20
:
: PRIOR APPLICATION NUMBER: 09/432,768
: PRIOR FILING DATE: 1999-11-03
:
: PRIOR APPLICATION NUMBER: 60/032,432
: PRIOR FILING DATE: 1996-12-05
:
: NUMBER OF SEQ ID NOS: 22
:
: SOFTWARE: PatentIn Ver. 2.0
:
: SEQ ID NO 21
:
: LENGTH: 46
:
: TYPE: DNA
:
: ORGANISM: Homo sapiens
:
: US-09-908-599-21

```

```

Query      1  CCCGGAGGCGAGTCTG  16
           |||||  |||||
Db          46  CCAGGAGTGCAGTCTG  31

      Query Match      62.2%; Score 11.2; DB 10; Length 46;
      Best Local Similarity 81.2%; Pred. No. 4, 8e+03;
      Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 38
US-09-817-487A-6/c
; Sequence 6, Application US/09817487A
; Patent No. US20020150876A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020150876A1artis AG
; TITLE OF INVENTION: Selectable Marker Genes
; FILE REFERENCE: 4-31193A

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1 CURRENT APPLICATION NUMBER: US-09/817,487A
2 CURRENT FILING DATE: 2002-02-14
3 NUMBER OF SEQ. ID NOS.: 10
4 SOFTWARE: patentIn version 3.0
5 SEQ. ID NO. 6
6
7 LENGTH: 27
8
9 TYPE: DNA
10
11 ORGANISM: homo sapiens
12
13 US-09-817-487A-6

```

Query Match	61.1%;	Score 11;	DB 10;	Length 27;
Best Local Similarity	100.0%;	Pred. No. 5.8e+03;		
Matches 11; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

OY	8	GGCAGTCTGGC	1
Db	1.9	GGCAGTCTGGC	9

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RESULT 39
US-09-866-108-1469
/ Sequence 1469, Application US/09866108
/ Patent No. US20020048000A1
/ GENERAL INFORMATION:
/ APPLICANT: GU, Yizhong
/ APPLICANT: JI, Yonggang
/ APPLICANT: PENN, Sharon G.
/ APPLICANT: HANZEL, David K.
/ APPLICANT: RANK, David R.
/ APPLICANT: CHEN, Wensheng
/ APPLICANT: SHANNON, Mark
/ TITLE OF INVENTION: MYO-SIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
/ FILE REFERENCE: AEOmica-7
/ CURRENT APPLICATION NUMBER: US/09/866,108
/ CURRENT FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00661
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00670
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US 60/266,860
/ PRIOR FILING DATE: 2001-02-05
/ NUMBER OF SEQ ID NOS: 15752
/ SOFTWARE: AeoMica Sequence Listing Engine
/ SEQ ID NO 1469
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-09-866-108-1469

```

Job time : 59 secs

Query Match 60.0%: Score 10.8; DB 10: Length 17;
Best Local Similarity 85.7%: Pred. No. 7, 1e+03;
Matches 12: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGAAGGAGCTGCG 17
||||| |||||
DB 4 GGAAGGAGGCTGC 17

RESULT 40

US-09-866-108-1473
Sequence 1473, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 1473
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-1473

Query Match 60.0%: Score 10.8; DB 10: Length 17;
Best Local Similarity 85.7%: Pred. No. 7, 1e+03;
Matches 12: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GAAGGAGCTGCG 18
||||| |||||
DB 1 GAAGGAGGCTGC 14

Search completed: December 2, 2002, 15:02:17

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 2, 2002, 12:42:48 ; Search time 1922 Seconds
(without alignments)
151.675 Million cell updates/sec

Title: US-09-848-868-35

Perfect score: 18

Sequence: 1 cccggaagcagctctgc 18

Scoring table: IDENTITY-NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

EST:*
1: em_estha:*
2: em_esthm:*
3: em_estln:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_rtn:*
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26: em_gss_rtn:*
27: em_gss_rtn:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13.4	74.4	43	9	A1786712 u56b03.x
2	13.2	73.3	40	9	A1113398 mp10f06.1
3	12.2	67.8	36	13	B1246232 602958773
4	12.2	67.8	50	9	AU104269 AU104269
5	11.8	65.6	42	17	A2824475 2M0095001
6	11.8	65.6	42	9	AA975650 oq63d09.s

7	11.8	65.6	45	17	A2815319	A2815319 2M0083A05
8	11.6	64.4	42	13	B1252223	B1252223 602953127
9	11.6	64.4	42	13	B1252484	B1252484 602952948
10	11.6	64.4	45	17	CNS07HVN	AL611573 Anopheles
11	11.6	64.4	50	9	AU102427	AU102427 AU102427
12	11.6	64.4	50	9	AU102430	AU102430 AU102430
13	11.6	64.4	50	9	AU102431	AU102431 AU102431
14	11.2	62.2	22	17	A2821049	A2821049 2M0093G07
15	11.2	62.2	22	17	A2776661	A2776661 2M0010C05
16	11.2	62.2	50	9	AU104235	AU104235 AU104235
17	11.2	62.2	50	9	AU104249	AU104249 AU104249
18	11.2	62.2	50	9	AU107261	AU107261 AU107261
19	10.8	60.0	38	17	A2874759	A2874759 2M0249E02
20	10.8	60.0	42	17	A2911289	A2911289 2M0275119
21	10.8	60.0	43	17	AL771267	AL771267 Arabidops
22	10.8	60.0	46	14	W05609	W05609 za85f01.r1
23	10.8	60.0	49	9	AA863626	AA863626 vx06b04.r
24	10.8	60.0	49	14	R82988	R82988 ypi0f11.r1
25	10.8	60.0	59	17	AU107138	AU107138 AU107138
26	10.6	58.9	29	17	A2610133	A2610133 1M0435E16
27	10.6	58.9	31	14	T62015	T62015 yb97c06.r1
28	10.6	58.9	38	17	A2953906	A2953906 2M0219B22
29	10.6	58.9	42	17	AQ939867	AQ939867 hmbx9s13
30	10.6	58.9	42	17	A2770047	A2770047 1M0571B19
31	10.6	58.9	43	14	H63217	H63217 yf48f07.r1
32	10.6	58.9	49	9	AA013635	AA013635 m12a02.r
33	10.6	58.9	49	9	A1185949	A1185949 qe29c04.s
34	10.6	58.9	50	9	AU108079	AU108079 AU108079
35	10.6	58.9	50	12	BG296675	BG296675 602933670
36	10.4	57.8	22	17	A2486623	A2486623 1M0314G14
37	10.4	57.8	33	17	A2595064	A2595064 1M0407D23
38	10.4	57.8	33	17	A2318942	A2318942 1M0038L15
39	10.4	57.8	35	17	A2313241	A2313241 1M0029H15
40	10.4	57.8	35	17	A2607760	A2607760 1M0430F22
41	10.4	57.8	46	9	AA846083	AA846083 ak79h06.s
42	10.4	57.8	49	9	AA561711	AA561711 v135e04.r
43	10.4	57.8	50	9	AU102385	AU102385 AU102385
44	10.4	57.8	50	9	AU102393	AU102393 AU102393
45	10.2	56.7	20	17	A2592714	A2592714 1M0403P13
46	10.2	56.7	21	17	A2789335	A2789335 2M0037B01
47	10.2	56.7	22	17	AA861441	AA861441 ak23h03.s
48	10.2	56.7	22	17	A2794867	A2794867 2M0048O15
49	10.2	56.7	37	17	AA969041	AA969041 op43d06.s
50	10.2	56.7	37	17	A2643581	A2643581 1M0507B10
51	10.2	56.7	38	17	A2786726	A2786726 2M0032H20
52	10.2	56.7	43	14	H23322	H23322 y136d09.r1
53	10.2	56.7	44	10	AV833341	AV833341 AV833341
54	10.2	56.7	46	9	BH865617	BH865617 SNK.0990
55	10.2	56.7	46	9	AA990254	AA990254 u62D12.15
56	10.2	56.7	47	12	B6777442	B6777442 602864745
57	10.2	56.7	49	17	A2658888	A2658888 1M0353J21
58	10.2	56.7	50	9	AU102426	AU102426 AU102426
59	10.2	56.7	50	9	AU103035	AU103035 AU103035
60	10.2	56.7	50	9	AU104159	AU104159 AU104159
61	10.2	56.7	50	9	AU105317	AU105317 AU105317
62	10.2	56.7	50	9	AU105506	AU105506 AU105506
63	10.2	56.7	50	9	AU105507	AU105507 AU105507
64	10.2	56.7	50	9	AU107902	AU107902 AU107902
65	10.2	56.7	25	9	AA880161	AA880161 vv96h04.r
66	10.2	56.7	34	9	AA978160	AA978160 ny36c03.s
67	10.2	56.7	36	17	A1364208	A1364208 gw35h11.x
68	10.2	56.7	36	17	A2477000	A2477000 1M0296D18
69	10.2	56.7	38	17	A2782406	A2782406 zw33b08.s
70	10.2	56.7	39	17	A2443133	A2443133 2M0022N12
71	10.2	56.7	41	17	A2470576	A2470576 1M0284B14
72	10.2	56.7	42	17	BH643860	BH643860 100896D05
73	10.2	56.7	44	17	A2448811	A2448811 1M0236C14
74	10.2	56.7	45	10	AM245471	AM245471 2822749.r
75	10.2	56.7	45	17	DR6115S	AL746188 Dania fer
76	10.2	56.7	46	17	A2660484	A2660484 1M0538P03
77	10.2	56.7	46	17	DA5789	DA5789 HDMS03003
78	10.2	56.7	46	17	DA5789	DA5789 HDMS03003
79	10.2	56.7	46	17	DA5789	DA5789 HDMS03003

80	10	55.6	49	9	AL775526	AL775526	AL775526	153	9.6	53.3	49	9	AA110365	AA110365 m195f03.r
C 81	10	55.6	49	14	C20870	C20870	C20870	154	9.6	53.3	49	9	AA501119	AA501119 vF97h07.r
82	10	55.6	49	14	W77746	W77746	W77746	155	9.6	53.3	49	13	BM284293	BM284293 k132h07.y
83	10	55.6	50	9	AUI03727	AUI03727	AUI03727	156	9.6	53.3	49	17	TA178E05Q	TA178E05Q
84	10	55.6	50	9	AUI04217	AUI04217	AUI04217	157	9.6	53.3	50	9	AUI02828	AUI02828 T. brucei
85	10	55.6	50	9	AUI04219	AUI04219	AUI04219	158	9.6	53.3	50	9	AUI02829	AUI02829
86	10	55.6	50	9	AUI05788	AUI05788	AUI05788	159	9.6	53.3	50	9	AUI03006	AUI03006
C 87	10	55.6	50	9	AUI06288	AUI06288	AUI06288	160	9.6	53.3	50	9	AUI03166	AUI03166
C 88	10	55.6	50	9	AUI06292	AUI06292	AUI06292	161	9.6	53.3	50	9	AUI03373	AUI03373
C 89	10	55.6	50	9	AUI07361	AUI07361	AUI07361	162	9.6	53.3	50	9	AUI03889	AUI03889
C 90	10	55.6	50	9	AUI08009	AUI08009	AUI08009	163	9.6	53.3	50	9	AUI04945	AUI04945
C 91	10	55.6	50	10	BB616279	BB616279	BB616279	164	9.6	53.3	50	9	AUI0584	AUI0584
C 92	10	55.6	22	17	AZ776605	AZ776605	AZ776605	165	9.6	53.3	50	9	AUI05859	AUI05859
C 93	9.8	54.4	23	17	AZ659392	AZ659392	AZ659392	166	9.6	53.3	50	9	AUI06634	AUI06634
C 94	9.8	54.4	25	17	BH854637	BH854637	BH854637	167	9.6	53.3	50	9	AUI06636	AUI06636
C 95	9.8	54.4	28	17	AA916534	AA916534	AA916534	168	9.6	53.3	50	9	AUI07987	AUI07987
C 96	9.8	54.4	38	17	AZ440668	AZ440668	AZ440668	169	9.6	53.3	50	9	AUI07988	AUI07988
C 97	9.8	54.4	39	17	AZ592385	AZ592385	AZ592385	170	9.6	53.3	50	9	AUI07996	AUI07996
C 98	9.8	54.4	39	17	AZ592385	AZ592385	AZ592385	171	9.6	53.3	50	14	T82724	T82724
C 99	9.8	54.4	40	9	AA990516	AA990516	AA990516	172	9.4	52.2	22	17	AZ372259	AZ372259
C 100	9.8	54.4	42	10	AV833675	AV833675	AV833675	173	9.4	52.2	26	17	AZ62630	AZ62630
C 101	9.8	54.4	44	9	AZ56664	AZ56664	AZ56664	174	9.4	52.2	27	17	AZ792197	AZ792197
C 102	9.8	54.4	44	12	BF792517	BF792517	BF792517	175	9.4	52.2	28	17	AZ759986	AZ759986
C 103	9.8	54.4	44	13	BT106206	BT106206	BT106206	176	9.4	52.2	30	17	AZ637716	AZ637716
C 104	9.8	54.4	44	17	AZ814521	AZ814521	AZ814521	177	9.4	52.2	34	13	B1690808	B1690808
C 105	9.8	54.4	46	17	AZ501017	AZ501017	AZ501017	178	9.4	52.2	36	12	B6699624	B6699624
C 106	9.8	54.4	48	17	AZ77915	AZ77915	AZ77915	179	9.4	52.2	37	9	AA680722	AA680722
C 107	9.8	54.4	48	17	BH866303	BH866303	BH866303	180	9.4	52.2	37	17	AZ312298	AZ312298
C 108	9.8	54.4	49	9	AA154153	AA154153	AA154153	181	9.4	52.2	37	17	AZ662400	AZ662400
C 109	9.8	54.4	49	17	AZ606700	AZ606700	AZ606700	182	9.4	52.2	39	9	AL787864	AL787864
C 110	9.8	54.4	50	9	AUI03386	AUI03386	AUI03386	183	9.4	52.2	39	17	AZ312458	AZ312458
C 111	9.8	54.4	50	9	AUI03856	AUI03856	AUI03856	184	9.4	52.2	40	17	AZ664676	AZ664676
C 112	9.8	54.4	50	9	AUI04350	AUI04350	AUI04350	185	9.4	52.2	40	17	AL770086	AL770086
C 113	9.8	54.4	50	9	AUI07388	AUI07388	AUI07388	186	9.4	52.2	41	17	AZ658005	AZ658005
C 114	9.8	54.4	50	9	AUI07901	AUI07901	AUI07901	187	9.4	52.2	41	17	AZ663826	AZ663826
C 115	9.8	54.4	50	9	AUI08030	AUI08030	AUI08030	188	9.4	52.2	42	13	B049432	B049432
C 116	9.8	54.4	50	9	AUI08031	AUI08031	AUI08031	189	9.4	52.2	43	13	B6701002	B6701002
C 117	9.8	54.4	50	9	AUI08032	AUI08032	AUI08032	190	9.4	52.2	46	9	AU259626	AU259626
C 118	9.8	54.4	50	10	AA249795	AA249795	AA249795	191	9.4	52.2	47	17	AZ845343	AZ845343
C 119	9.8	54.4	50	17	AZ781441	AZ781441	AZ781441	192	9.4	52.2	47	17	TA132E04P	TA132E04P
C 120	9.8	54.4	50	17	BH644632	BH644632	BH644632	193	9.4	52.2	49	9	AA157965	AA157965
C 121	9.8	54.4	50	17	BH847539	BH847539	BH847539	194	9.4	52.2	50	9	AUI02826	AUI02826
C 122	9.6	53.3	22	9	AA911591	AA911591	AA911591	195	9.4	52.2	50	9	AUI03596	AUI03596
C 123	9.6	53.3	23	17	AZ822715	AZ822715	AZ822715	196	9.4	52.2	50	9	AUI03598	AUI03598
C 124	9.6	53.3	24	17	AZ449783	AZ449783	AZ449783	197	9.4	52.2	50	9	AUI04493	AUI04493
C 125	9.6	53.3	26	17	AZ623015	AZ623015	AZ623015	198	9.4	52.2	50	9	AUI04699	AUI04699
C 126	9.6	53.3	28	9	AA856526	AA856526	AA856526	199	9.4	52.2	50	9	AUI05508	AUI05508
C 127	9.6	53.3	28	9	AA484974	AA484974	AA484974	200	9.4	52.2	50	9	AUI05633	AUI05633
C 128	9.6	53.3	28	17	BH848015	BH848015	BH848015	201	9.4	52.2	50	9	AUI06503	AUI06503
C 129	9.6	53.3	31	9	AA193525	AA193525	AA193525	202	9.4	52.2	50	9	AUI06751	AUI06751
C 130	9.6	53.3	32	14	T67801	T67801	T67801	203	9.4	52.2	50	9	AUI06753	AUI06753
C 131	9.6	53.3	33	12	BG529354	BG529354	BG529354	204	9.4	52.2	50	9	AUI06755	AUI06755
C 132	9.6	53.3	34	17	AZ491280	AZ491280	AZ491280	205	9.4	52.2	50	9	AUI06758	AUI06758
C 133	9.6	53.3	37	9	AUI240580	AUI240580	AUI240580	206	9.4	52.2	50	9	AUI06759	AUI06759
C 134	9.6	53.3	37	17	AZ476475	AZ476475	AZ476475	207	9.4	52.2	50	9	AUI06764	AUI06764
C 135	9.6	53.3	39	17	AZ666463	AZ666463	AZ666463	208	9.4	52.2	50	9	AUI07406	AUI07406
C 136	9.6	53.3	40	9	AA213154	AA213154	AA213154	209	9.4	52.2	50	9	AUI07665	AUI07665
C 137	9.6	53.3	40	17	AZ310280	AZ310280	AZ310280	210	9.4	52.2	50	9	AUI07667	AUI07667
C 138	9.6	53.3	41	12	B07643	B07643	B07643	211	9.4	52.2	50	9	AUI07669	AUI07669
C 139	9.6	53.3	41	12	BG718339	BG718339	BG718339	212	9.4	52.2	50	14	R98157	R98157
C 140	9.6	53.3	41	13	BT465330	BT465330	BT465330	213	9.4	52.2	50	17	AZ481318	AZ481318
C 141	9.6	53.3	42	14	T51284	T51284	T51284	214	9.4	52.2	50	17	BH639080	BH639080
C 142	9.6	53.3	42	17	AZ654954	AZ654954	AZ654954	215	9.2	51.1	22	17	AZ324102	AZ324102
C 143	9.6	53.3	43	13	AA231049	AA231049	AA231049	216	9.2	51.1	23	17	AZ806883	AZ806883
C 144	9.6	53.3	43	13	BT333375	BT333375	BT333375	217	9.2	51.1	23	17	TA619040	TA619040
C 145	9.6	53.3	43	17	AZ447897	AZ447897	AZ447897	218	9.2	51.1	24	17	AZ586934	AZ586934
C 146	9.6	53.3	43	17	TA84B020	TA84B020	TA84B020	219	9.2	51.1	24	17	AZ982483	AZ982483
C 147	9.6	53.3	44	9	AA930614	AA930614	AA930614	220	9.2	51.1	27	17	AZ468814	AZ468814
C 148	9.6	53.3	45	17	AZ862434	AZ862434	AZ862434	221	9.2	51.1	27	17	AZ598057	AZ598057
C 149	9.6	53.3	45	17	BH848090	BH848090	BH848090	222	9.2	51.1	28	9	AA871664	AA871664
C 150	9.6	53.3	46	9	AA182146	AA182146	AA182146	223	9.2	51.1	28	9	AZ769631	AZ769631
C 151	9.6	53.3	47	10	BH534847	BH534847	BH534847	224	9.2	51.1	28	17	AZ492195	AZ492195
C 152	9.6	53.3	49	9	AA103183	AA103183	AA103183	225	9.2	51.1	29	17	AZ759919	AZ759919

226	9.2	51.1	30	17	Az498972	AZ498972	1M0336D06	C 299	9.2	51.1	50	9	AU106746	AU106746	AU106746
C 227	9.2	51.1	30	17	AZ658025	AZ658025	1M0534N04	C 300	9.2	51.1	50	9	AU106749	AU106749	AU106749
C 228	9.2	51.1	31	17	AZ402417	AZ402417	1M0169008	C 301	9.2	51.1	50	9	AU107180	AU107180	AU107180
C 229	9.2	51.1	31	17	AZ407129	AZ407129	1M0176K10	C 302	9.2	51.1	50	9	AU107596	AU107596	AU107596
C 230	9.2	51.1	32	13	BZ033001	BZ033001	BZ033001	C 303	9.2	51.1	50	9	AU107670	AU107670	AU107670
C 231	9.2	51.1	32	14	T49101	T49101	Yb08h11_r1	C 304	9.2	51.1	50	9	AA250719	AA250719	AA250719
C 232	9.2	51.1	32	17	AZ339655	AZ339655	1M0071A13	C 305	9.2	51.1	50	9	AA233215	AA233215	AA233215
C 233	9.2	51.1	32	12	AZ618803	AZ618803	1M0450F13	C 306	9.2	51.1	50	9	AZ653501	AZ653501	AZ653501
C 234	9.2	51.1	33	13	BZ073398	BZ073398	602335701	C 307	9.2	51.1	50	9	AZ624350	AZ624350	AZ624350
C 235	9.2	51.1	33	13	BZ082442	BZ082442	602335701	C 308	9.2	51.1	50	9	R89803	R89803	R89803
C 236	9.2	51.1	33	17	AZ438620	AZ438620	1M0238106	C 309	9.2	51.1	50	9	TA296B02Q	TA296B02Q	TA296B02Q
C 237	9.2	51.1	33	17	AZ780229	AZ780229	2M0017G24	C 310	9.2	51.1	50	9	AZ978415	AZ978415	AZ978415
C 238	9.2	51.1	33	17	TA247408Q	TA247408Q	AL488059_r1_bruce1	C 311	9.2	51.1	50	9	AZ978415	AZ978415	AZ978415
C 239	9.2	51.1	33	17	TA263603P	TA263603P	AL488059_r1_bruce1	C 312	9.2	51.1	50	9	AZ978415	AZ978415	AZ978415
C 240	9.2	51.1	34	9	A1188358	A1188358	qd08c03_r	C 313	9.2	51.1	50	9	AZ476559	AZ476559	AZ476559
C 241	9.2	51.1	34	9	AA259780	AA259780	va87b10_r	C 314	9.2	51.1	50	9	BH011395	BH011395	BH011395
C 242	9.2	51.1	34	14	N73483	N73483	za05h02_s1	C 315	9.2	51.1	50	9	AZ433900	AZ433900	AZ433900
C 243	9.2	51.1	35	17	AZ647296	AZ647296	1M0513A16	C 316	9.2	51.1	50	9	AZ591789	AZ591789	AZ591789
C 244	9.2	51.1	35	17	AZ780266	AZ780266	2M0017O21	C 317	9.2	51.1	50	9	AA685943	AA685943	AA685943
C 245	9.2	51.1	36	10	AV950606	AV950606	AV950606	C 318	9.2	51.1	50	9	A1698994	A1698994	A1698994
C 246	9.2	51.1	36	14	C00778	C00778	HUMGS000239	C 319	9.2	51.1	50	9	A1698994	A1698994	A1698994
C 247	9.2	51.1	37	9	A1917811	A1917811	wb53c07_r	C 320	9.2	51.1	50	9	A2348137	A2348137	A2348137
C 248	9.2	51.1	37	17	AZ810046	AZ810046	2M0074C23	C 321	9.2	51.1	50	9	AZ676784	AZ676784	AZ676784
C 249	9.2	51.1	37	17	TA325G09P	TA325G09P	AL499086_r1_bruce1	C 322	9.2	51.1	50	9	B1151368	B1151368	B1151368
C 250	9.2	51.1	39	12	BP032106	BP032106	601559566	C 323	9.2	51.1	50	9	B1066180	B1066180	B1066180
C 251	9.2	51.1	39	14	D26027	D26027	HUMGS02394	C 324	9.2	51.1	50	9	AZ654189	AZ654189	AZ654189
C 252	9.2	51.1	39	17	AZ331571	AZ331571	1M0059N06	C 325	9.2	51.1	50	9	AZ779073	AZ779073	AZ779073
C 253	9.2	51.1	39	17	AZ242459	AZ242459	1M0203D07	C 326	9.2	51.1	50	9	AZ602844	AZ602844	AZ602844
C 254	9.2	51.1	39	17	AZ862477	AZ862477	2M0268J20	C 327	9.2	51.1	50	9	AB016905	AB016905	AB016905
C 255	9.2	51.1	40	10	AV834421	AV834421	AV834421	C 328	9.2	51.1	50	9	AA929647	AA929647	AA929647
C 256	9.2	51.1	40	13	B1546135	B1546135	603188514	C 329	9.2	51.1	50	9	AA936967	AA936967	AA936967
C 257	9.2	51.1	41	10	AV955327	AV955327	AV955327	C 330	9.2	51.1	50	9	A1142664	A1142664	A1142664
C 258	9.2	51.1	41	9	AA907625	AA907625	cm10e08_s	C 331	9.2	51.1	50	9	A1744372	A1744372	A1744372
C 259	9.2	51.1	43	17	AZ645943	AZ645943	1M0080M23	C 332	9.2	51.1	50	9	A1788546	A1788546	A1788546
C 260	9.2	51.1	43	17	AZ663363	AZ663363	1M0542021	C 333	9.2	51.1	50	9	AA173155	AA173155	AA173155
C 261	9.2	51.1	44	17	BH635056	BH635056	100800J21	C 334	9.2	51.1	50	9	AV833436	AV833436	AV833436
C 262	9.2	51.1	44	17	AZ787976	AZ787976	2M0043J15	C 335	9.2	51.1	50	9	B1179705	B1179705	B1179705
C 263	9.2	51.1	45	10	AV833283	AV833283	AV833283	C 336	9.2	51.1	50	9	AZ352753	AZ352753	AZ352753
C 264	9.2	51.1	45	12	BE907096	BE907096	601500842	C 337	9.2	51.1	50	9	AZ486062	AZ486062	AZ486062
C 265	9.2	51.1	45	17	AZ662097	AZ662097	1M0541D03	C 338	9.2	51.1	50	9	AZ821491	AZ821491	AZ821491
C 266	9.2	51.1	46	9	A1203788	A1203788	qf77b04_r	C 339	9.2	51.1	50	9	BC765238	BC765238	BC765238
C 267	9.2	51.1	46	9	A1431214	A1431214	sa22a01_r	C 340	9.2	51.1	50	9	AZ328039	AZ328039	AZ328039
C 268	9.2	51.1	46	14	N77017	N77017	yz83b09_r1	C 341	9.2	51.1	50	9	AA037578	AA037578	AA037578
C 269	9.2	51.1	46	17	AZ815494	AZ815494	2M0083C18	C 342	9.2	51.1	50	9	A1303673	A1303673	A1303673
C 270	9.2	51.1	49	9	A1416542	A1416542	sa10e02_r	C 343	9.2	51.1	50	9	A1889861	A1889861	A1889861
C 271	9.2	51.1	49	9	A1875730	A1875730	ue63g05_r	C 344	9.2	51.1	50	9	BM398993	BM398993	BM398993
C 272	9.2	51.1	49	9	A1875730	A1875730	u124b01_x	C 345	9.2	51.1	50	9	AQ025713	AQ025713	AQ025713
C 273	9.2	51.1	49	10	AV960885	AV960885	AV960885	C 346	9.2	51.1	50	9	AZ648627	AZ648627	AZ648627
C 274	9.2	51.1	49	17	AZ309933	AZ309933	1M0017G23	C 347	9.2	51.1	50	9	HSWC09A10	HSWC09A10	HSWC09A10
C 275	9.2	51.1	50	9	AA114351	AA114351	MBAPCE4A0	C 348	9.2	51.1	50	9	TA115G06P	TA115G06P	TA115G06P
C 276	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 349	9.2	51.1	50	9	AL637555	AL637555	AL637555
C 277	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 350	9.2	51.1	50	9	BJ060923	BJ060923	BJ060923
C 278	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 351	9.2	51.1	50	9	AL637555	AL637555	AL637555
C 279	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 352	9.2	51.1	50	9	AL637555	AL637555	AL637555
C 280	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 353	9.2	51.1	50	9	AL637555	AL637555	AL637555
C 281	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 354	9.2	51.1	50	9	AL637555	AL637555	AL637555
C 282	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 355	9.2	51.1	50	9	AL637555	AL637555	AL637555
C 283	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 356	9.2	51.1	50	9	AL637555	AL637555	AL637555
C 284	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 357	9.2	51.1	50	9	AL637555	AL637555	AL637555
C 285	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 358	9.2	51.1	50	9	AL637555	AL637555	AL637555
C 286	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 359	9.2	51.1	50	9	AL637555	AL637555	AL637555
C 287	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 360	9.2	51.1	50	9	AL637555	AL637555	AL637555
C 288	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 361	9.2	51.1	50	9	AL637555	AL637555	AL637555
C 289	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 362	9.2	51.1	50	9	AL637555	AL637555	AL637555
C 290	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 363	9.2	51.1	50	9	AL637555	AL637555	AL637555
C 291	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 364	9.2	51.1	50	9	AL637555	AL637555	AL637555
C 292	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 365	9.2	51.1	50	9	AL637555	AL637555	AL637555
C 293	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 366	9.2	51.1	50	9	AL637555	AL637555	AL637555
C 294	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 367	9.2	51.1	50	9	AL637555	AL637555	AL637555
C 295	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 368	9.2	51.1	50	9	AL637555	AL637555	AL637555
C 296	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 369	9.2	51.1	50	9	AL637555	AL637555	AL637555
C 297	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 370	9.2	51.1	50	9	AL637555	AL637555	AL637555
C 298	9.2	51.1	50	9	AJ283030	AJ283030	4A3A-P4A1	C 371	9.2	51.1	50	9	AL637555	AL637555	AL637555

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373	9	50.0	43	9	AA564874	AA564874 nj01b02.s	446	9	50.0	50	9	AU107356	AU107356
374	9	50.0	43	14	H79092	H79092 yv77c12.s1	447	9	50.0	50	9	AU107358	AU107358
375	9	50.0	43	14	R71759	R71759 y185d09.s1	448	9	50.0	50	9	AU107359	AU107359
376	9	50.0	43	17	A2771147	A2771147 IM0573b07	449	9	50.0	50	9	AU107366	AU107366
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379	9	50.0	45	13	BJ015280	BJ015280 BJ015280	452	9	50.0	50	9	AU107369	AU107369
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384	9	50.0	46	9	A1003237	A1003237 an11h01.s	457	9	50.0	50	9	AU107375	AU107375
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386	9	50.0	46	9	A1159160	A1159160 vz8hail1.r	459	9	50.0	50	9	AU107377	AU107377
387	9	50.0	46	9	A1590143	A1590143 tol2e12.x	460	9	50.0	50	9	AU107378	AU107378
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390	9	50.0	47	13	B1412781	B1412781 602988478	463	9	50.0	50	9	AU107410	AU107410
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392	9	50.0	47	17	TA67C120	TA67C120 T. brucei	465	9	50.0	50	9	AU107415	AU107415
393	9	50.0	47	17	TA96H120	TA96H120 T. brucei	466	9	50.0	50	9	AU107423	AU107423
394	9	50.0	48	17	A2601433	A2601433 IM0419N11	467	9	50.0	50	9	AU107425	AU107425
395	9	50.0	48	17	A2601433	A2601433 IM0419N11	468	9	50.0	50	9	AU107425	AU107425
396	9	50.0	49	9	A1147960	A1147960 q962c04.s	469	9	50.0	50	9	AU107592	AU107592
397	9	50.0	49	9	A1709135	A1709135 as62g01.x	470	9	50.0	50	9	AU107601	AU107601
398	9	50.0	49	9	AL785672	AL785672	471	9	50.0	50	9	AU107602	AU107602
399	9	50.0	49	9	AA233385	AA233385 zr28a05.r	472	9	50.0	50	9	AU107762	AU107762
400	9	50.0	49	12	BF984179	BF984179 602306891	473	9	50.0	50	9	AU107913	AU107913
401	9	50.0	49	13	B1518984	B1518984 603062281	474	9	50.0	50	12	BG31S187	BG31S187
402	9	50.0	49	14	C01065	C01065 HOMGS000770	475	9	50.0	50	14	R85071	R85071
403	9	50.0	49	14	H46153	H46153 y013e12.r1	476	9	50.0	50	17	A2452909	A2452909
404	9	50.0	49	14	T74948	T74948 yC58b12.r1	477	9	50.0	50	17	A29449090	A29449090
405	9	50.0	49	17	A2481961	A2481961 IM0306h07	478	9	48.9	20	17	A2611227	A2611227
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407	9	50.0	49	17	A2604991	A2604991 IM0426R11	480	9	48.9	22	9	A1080445	A1080445
408	9	50.0	49	17	A2615333	A2615333 IM0444D09	481	9	48.9	22	9	A1080445	A1080445
409	9	50.0	50	9	AU102600	AU102600 AU102600	482	9	48.9	23	17	A2482703	A2482703
410	9	50.0	50	9	AU102767	AU102767 AU102767	483	9	48.9	25	17	A2790354	A2790354
411	9	50.0	50	9	AU102839	AU102839 AU102839	484	9	48.9	25	17	BH865645	BH865645
412	9	50.0	50	9	AU102888	AU102888 AU102888	485	9	48.9	25	17	TA188E10P	TA188E10P
413	9	50.0	50	9	AU103386	AU103386 AU103386	486	9	48.9	26	14	H25839	H25839
414	9	50.0	50	9	AU103585	AU103585 AU103585	487	9	48.9	28	17	A2491585	A2491585
415	9	50.0	50	9	AU103585	AU103585 AU103585	488	9	48.9	29	17	A2488981	A2488981
416	9	50.0	50	9	AU103683	AU103683 AU103683	489	9	48.9	29	17	A2803250	A2803250
417	9	50.0	50	9	AU103696	AU103696 AU103696	490	9	48.9	30	17	A2655716	A2655716
418	9	50.0	50	9	AU104228	AU104228 AU104228	491	9	48.9	31	17	A2478840	A2478840
419	9	50.0	50	9	AU104229	AU104229 AU104229	492	9	48.9	32	12	BG115925	BG115925
420	9	50.0	50	9	AU104230	AU104230 AU104230	493	9	48.9	32	13	BJ052038	BJ052038
421	9	50.0	50	9	AU104231	AU104231 AU104231	494	9	48.9	32	17	A2453644	A2453644
422	9	50.0	50	9	AU104233	AU104233 AU104233	495	9	48.9	33	17	A2772019	A2772019
423	9	50.0	50	9	AU104265	AU104265 AU104265	496	9	48.9	33	17	A2781232	A2781232
424	9	50.0	50	9	AU104267	AU104267 AU104267	497	9	48.9	34	9	A1073612	A1073612
425	9	50.0	50	9	AU104268	AU104268 AU104268	498	9	48.9	34	9	AU255522	AU255522
426	9	50.0	50	9	AU104270	AU104270 AU104270	499	9	48.9	34	14	R96723	R96723
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428	9	50.0	50	9	AU104273	AU104273 AU104273	501	9	48.9	34	17	A2313905	A2313905
429	9	50.0	50	9	AU104286	AU104286 AU104286	502	9	48.9	35	9	AU007015	AU007015
430	9	50.0	50	9	AU104765	AU104765 AU104765	503	9	48.9	35	9	AU007016	AU007016
431	9	50.0	50	9	AU104963	AU104963 AU104963	504	9	48.9	35	17	A2604061	A2604061
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435	9	50.0	50	9	AU105451	AU105451 AU105451	508	9	48.9	37	9	A1917811	A1917811
436	9	50.0	50	9	AU105855	AU105855 AU105855	509	9	48.9	37	9	A1918224	A1918224
437	9	50.0	50	9	AU105890	AU105890 AU105890	510	9	48.9	37	17	BH810697	BH810697
438	9	50.0	50	9	AU106018	AU106018 AU106018	511	9	48.9	38	12	BG699164	BG699164
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441	9	50.0	50	9	AU106655	AU106655 AU106655	514	9	48.9	39	13	B1689793	B1689793
442	9	50.0	50	9	AU106763	AU106763 AU106763	515	9	48.9	39	13	BJ063725	BJ063725
443	9	50.0	50	9	AU107100	AU107100 AU107100	516	9	48.9	39	14	R77120	R77120
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518	8.8	48.9	40	9	A1376705	A1376705 tc29d03.x	C 591	8.8	48.9	50	9	AU102882	AU102882 AU102882
C 519	8.8	48.9	40	9	A197105	A197105 zq9h01.r	C 592	8.8	48.9	50	9	AU102886	AU102886 AU102886
C 520	8.8	48.9	40	9	AA616695	AA616695 vn67e02.r	C 593	8.8	48.9	50	9	AU102993	AU102993 AU102993
C 521	8.8	48.9	40	13	BJ060137	BJ060137 BJ060137	C 594	8.8	48.9	50	9	AU103237	AU103237 AU103237
C 522	8.8	48.9	40	17	BH809373	BH809373 1008089D1	C 595	8.8	48.9	50	9	AU103338	AU103338 AU103338
C 523	8.8	48.9	41	12	BG683582	BG683582 602651062	C 596	8.8	48.9	50	9	AU103339	AU103339 AU103339
C 524	8.8	48.9	41	17	AZ765135	AZ765135 1M0561123	C 597	8.8	48.9	50	9	AU103340	AU103340 AU103340
C 525	8.8	48.9	42	9	A1191530	A1191530 qe49a09.x	C 598	8.8	48.9	50	9	AU103342	AU103342 AU103342
C 526	8.8	48.9	43	9	AA680285	AA680285 ac66d06.x	C 599	8.8	48.9	50	9	AU103854	AU103854 AU103854
C 527	8.8	48.9	43	9	A1660376	A1660376 zc74b05.r	C 600	8.8	48.9	50	9	AU103857	AU103857 AU103857
C 528	8.8	48.9	43	9	AU256860	AU256860 AU256860	C 601	8.8	48.9	50	9	AU104073	AU104073 AU104073
C 529	8.8	48.9	43	9	AA495842	AA495842 zvc5a02.r	C 602	8.8	48.9	50	9	AU104074	AU104074 AU104074
C 530	8.8	48.9	43	17	AZ762861	AZ762861 1M0358P04	C 603	8.8	48.9	50	9	AU104356	AU104356 AU104356
C 531	8.8	48.9	44	17	BE367536	BE367536 601649333	C 604	8.8	48.9	50	9	AU104694	AU104694 AU104694
C 532	8.8	48.9	44	17	BH643282	BH643282 100805560	C 605	8.8	48.9	50	9	AU105582	AU105582 AU105582
C 533	8.8	48.9	45	12	BF691166	BF691166 602247257	C 606	8.8	48.9	50	9	AU105803	AU105803 AU105803
C 534	8.8	48.9	45	14	H91384	H91384 yu87h05.r1	C 607	8.8	48.9	50	9	AU105903	AU105903 AU105903
C 535	8.8	48.9	45	14	T92229	T92229 ye17f11.r1	C 608	8.8	48.9	50	9	AU106287	AU106287 AU106287
C 536	8.8	48.9	45	17	AZ328791	AZ328791 1M0052B18	C 609	8.8	48.9	50	9	AU106332	AU106332 AU106332
C 537	8.8	48.9	45	17	AZ791686	AZ791686 2M0041N10	C 610	8.8	48.9	50	9	AU106763	AU106763 AU106763
C 538	8.8	48.9	45	17	AZ806099	AZ806099 2M0067M20	C 611	8.8	48.9	50	9	AU106912	AU106912 AU106912
C 539	8.8	48.9	45	17	AZ806099	AZ806099 2M0067M20	C 612	8.8	48.9	50	9	AU107022	AU107022 AU107022
C 540	8.8	48.9	45	17	AA828900	AA828900 odt5h11.s	C 613	8.8	48.9	50	9	AU107087	AU107087 AU107087
C 541	8.8	48.9	46	9	AA836932	AA836932 of36c11.s	C 614	8.8	48.9	50	9	AU107092	AU107092 AU107092
C 542	8.8	48.9	46	9	AA916643	AA916643 oh81905.s	C 615	8.8	48.9	50	9	AU107257	AU107257 AU107257
C 543	8.8	48.9	46	9	A1323615	A1323615 mp73h09.x	C 616	8.8	48.9	50	9	AU107258	AU107258 AU107258
C 544	8.8	48.9	46	13	B1549257	B1549257 603189880	C 617	8.8	48.9	50	9	AU107259	AU107259 AU107259
C 545	8.8	48.9	46	13	BM393789	BM393789 50072-2-1	C 618	8.8	48.9	50	9	AU107260	AU107260 AU107260
C 546	8.8	48.9	46	14	M44070	M44070 yy30f05.r1	C 619	8.8	48.9	50	9	AU107543	AU107543 AU107543
C 547	8.8	48.9	46	14	R27270	R27270 yj35a01.r1	C 620	8.8	48.9	50	9	AU107621	AU107621 AU107621
C 548	8.8	48.9	46	14	W09482	W09482 ma07a09.r1	C 621	8.8	48.9	50	9	AU107622	AU107622 AU107622
C 549	8.8	48.9	46	14	W94066	W94066 zd98e11.s1	C 622	8.8	48.9	50	9	AU107623	AU107623 AU107623
C 550	8.8	48.9	46	17	AZ324779	AZ324779 1M0046D22	C 623	8.8	48.9	50	9	AU107685	AU107685 AU107685
C 551	8.8	48.9	46	17	AZ946179	AZ946179 2M0207D19	C 624	8.8	48.9	50	9	AU107687	AU107687 AU107687
C 552	8.8	48.9	46	9	AA642360	AA642360 ns29f08.s	C 625	8.8	48.9	50	9	AU107717	AU107717 AU107717
C 553	8.8	48.9	47	9	AA828450	AA828450 oc46d08.s	C 626	8.8	48.9	50	9	AU107718	AU107718 AU107718
C 554	8.8	48.9	47	10	BB619449	BB619449 601473280	C 627	8.8	48.9	50	9	AU107719	AU107719 AU107719
C 555	8.8	48.9	47	14	H82798	H82798 yq4b06.s1	C 628	8.8	48.9	50	9	AU107720	AU107720 AU107720
C 556	8.8	48.9	47	14	R63276	R63276 y107e04.r1	C 629	8.8	48.9	50	9	AU107721	AU107721 AU107721
C 557	8.8	48.9	47	17	AZ399403	AZ399403 1M0165C17	C 630	8.8	48.9	50	9	AU107722	AU107722 AU107722
C 558	8.8	48.9	47	17	AZ462142	AZ462142 1M0269K14	C 631	8.8	48.9	50	9	AU107723	AU107723 AU107723
C 559	8.8	48.9	47	17	AZ583296	AZ583296 1M0378G15	C 632	8.8	48.9	50	9	AU107724	AU107724 AU107724
C 560	8.8	48.9	47	17	AZ840029	AZ840029 2M0136F21	C 633	8.8	48.9	50	9	AU107857	AU107857 AU107857
C 561	8.8	48.9	48	17	BH618704	BH618704 SALK_0395	C 634	8.8	48.9	50	9	AU107927	AU107927 AU107927
C 562	8.8	48.9	48	17	AZ331129	AZ331129 1M0056M21	C 635	8.8	48.9	50	13	B1708833	B1708833 BF46C02.Y
C 563	8.8	48.9	48	17	AZ801205	AZ801205 2M0059N01	C 636	8.8	48.9	50	17	AZ325789	AZ325789 1M0037P02
C 564	8.8	48.9	48	17	BH890043	BH890043 3526.1-12	C 637	8.8	48.9	50	17	BH854860	BH854860 SALK_0861
C 565	8.8	48.9	49	9	A1020998	A1020998 ua98e05.r	C 638	8.8	48.9	50	17	AZ602332	AZ602332 1M0421104
C 566	8.8	48.9	49	9	AA328955	AA328955 nc14a06.r	C 639	8.8	48.9	50	17	TA119B07P	TA119B07P TA119B07P
C 567	8.8	48.9	49	12	BE592288	BE592288 602249170	C 640	8.8	48.9	50	17	TA119B07P	TA119B07P TA119B07P
C 568	8.8	48.9	49	13	BI770218	BI770218 603053284	C 641	8.8	48.9	50	17	TA119B07P	TA119B07P TA119B07P
C 569	8.8	48.9	49	13	BI910486	BI910486 603067855	C 642	8.8	48.9	50	17	TA119B07P	TA119B07P TA119B07P
C 570	8.8	48.9	49	14	W71090	W71090 me27h08.r1	C 643	8.8	48.9	50	17	TA119B07P	TA119B07P TA119B07P
C 571	8.8	48.9	49	14	W80511	W80511 zh50h08.r1	C 644	8.8	48.9	50	17	TA119B07P	TA119B07P TA119B07P
C 572	8.8	48.9	49	17	AZ397630	AZ397630 1M0162012	C 645	8.8	48.9	50	17	AA896882	AA896882 vy11d08.r
C 573	8.8	48.9	49	17	AZ465494	AZ465494 1M0275023	C 646	8.8	48.9	50	14	CO1243	CO1243 HUGS00796
C 574	8.8	48.9	49	17	AZ795452	AZ795452 2M0049M11	C 647	8.8	48.9	50	17	AZ424958	AZ424958 1M0011L06
C 575	8.8	48.9	49	17	AZ804582	AZ804582 2M0065009	C 648	8.8	48.9	50	17	AZ424958	AZ424958 1M0011L06
C 576	8.8	48.9	49	17	AZ804582	AZ804582 2M0065009	C 649	8.8	48.9	50	17	AZ424958	AZ424958 1M0011L06
C 577	8.8	48.9	49	17	AZ804582	AZ804582 2M0065009	C 650	8.8	48.9	50	17	AZ424958	AZ424958 1M0011L06
C 578	8.8	48.9	49	17	AZ804582	AZ804582 2M0065009	C 651	8.8	48.9	50	17	AZ424958	AZ424958 1M0011L06
C 579	8.8	48.9	49	17	AA937985	AA937985 2M0270F11	C 652	8.8	48.9	50	17	AZ424958	AZ424958 1M0011L06
C 580	8.8	48.9	50	9	AA937985	AA937985 2M0270F11	C 653	8.8	48.9	50	17	AZ424958	AZ424958 1M0011L06
C 581	8.8	48.9	50	9	AU102262	AU102262 AU102262	C 654	8.8	48.9	50	17	AZ424958	AZ424958 1M0011L06
C 582	8.8	48.9	50	9	AU102264	AU102264 AU102264	C 655	8.8	48.9	50	17	AZ424958	AZ424958 1M0011L06
C 583	8.8	48.9	50	9	AU102267	AU102267 AU102267	C 656	8.8	48.9	50	17	AZ424958	AZ424958 1M0011L06
C 584	8.8	48.9	50	9	AU102268	AU102268 AU102268	C 657	8.8	48.9	50	17	AZ424958	AZ424958 1M0011L06
C 585	8.8	48.9	50	9	AU102269	AU102269 AU102269	C 658	8.8	48.9	50	17	AZ424958	AZ424958 1M0011L06
C 586	8.8	48.9	50	9	AU102284	AU102284 AU102284	C 659	8.8	48.9	50	17	AZ424958	AZ424958 1M0011L06
C 587	8.8	48.9	50	9	AU102285	AU102285 AU102285	C 660	8.8	48.9	50	17	AZ424958	AZ424958 1M0011L06
C 588	8.8	48.9	50	9	AU102321	AU102321 AU102321	C 661	8.8	48.9	50	17	AZ424958	AZ424958 1M0011L06
C 589	8.8	48.9	50	9	AU102378	AU102378 AU102378	C 662	8.8	48.9	50	17	AZ424958	AZ424958 1M0011L06
C 590	8.8	48.9	50	9	AU102379	AU102379 AU102379	C 663	8.8	48.9	50	17	AZ424958	AZ424958 1M0011L06

664	8.6	47.8	31	17	A2481810	A2481810	1M0306C21	737	8.6	47.8	46	17	A2833980	A2833980	2M0116K21
665	8.6	47.8	31	17	A2620934	A2620934	1M0453B23	738	8.6	47.8	47	17	AA087264	AA087264	mol2f10.r
666	8.6	47.8	31	17	A2788442	A2788442	2M0035602	739	8.6	47.8	47	12	BG404659	BG404659	60242081.r
667	8.6	47.8	32	13	B1223057	B1223057	602942007	740	8.6	47.8	47	17	A2823060	A2823060	2M0096B22
668	8.6	47.8	32	13	B1664149	B1664149	603289266	741	8.6	47.8	47	17	BH840587	BH840587	KC05681-3
669	8.6	47.8	32	13	BJ032969	BJ032969	BJ032969	742	8.6	47.8	47	17	BL761639	BL761639	Arabidops
670	8.6	47.8	32	17	A2853979	A2853979	2M0157H21	743	8.6	47.8	48	17	AL767745	AL767745	Arabidops
671	8.6	47.8	33	17	AQ026498	AQ026498	EP(2)0755	744	8.6	47.8	49	9	AA233183	AA233183	z945f01.s
672	8.6	47.8	33	17	A2861593	A2861593	2M0168A09	745	8.6	47.8	49	9	AA233183	AA233183	z945f01.s
673	8.6	47.8	34	17	A2315997	A2315997	1M0033023	746	8.6	47.8	49	10	AM100845	AM100845	s662b05.Y
674	8.6	47.8	35	9	AL658499	AL658499	AL658499	747	8.6	47.8	49	14	C20877	C20877	HUMCS000494
675	8.6	47.8	35	10	BE553379	BE553379	601233117	748	8.6	47.8	49	14	RS5033	RS5033	y176f02.s1
676	8.6	47.8	35	17	A2775090	A2775090	2M0007002	749	8.6	47.8	49	17	A2817223	A2817223	2M0086N19
677	8.6	47.8	36	12	BE735658	BE735658	601304404	750	8.6	47.8	49	17	A2834261	A2834261	2M0116B19
678	8.6	47.8	36	17	AQ026010	AQ026010	EP(2)0461	751	8.6	47.8	49	17	A2850572	A2850572	2M0152B03
679	8.6	47.8	37	10	AA149901	AA149901	z002f05.r	752	8.6	47.8	50	9	AM102365	AM102365	AM102365
680	8.6	47.8	37	10	AM250607	AM250607	28322076.5	753	8.6	47.8	50	9	AM102372	AM102372	AM102372
681	8.6	47.8	37	14	B0605582	B0605582	BR_1070	754	8.6	47.8	50	9	AM102373	AM102373	AM102373
682	8.6	47.8	37	17	AQ025921	AQ025921	1(2)K1010	755	8.6	47.8	50	9	AM102375	AM102375	AM102375
683	8.6	47.8	37	17	A2384621	A2384621	1M0142A13	756	8.6	47.8	50	9	AM102744	AM102744	AM102744
684	8.6	47.8	37	17	TA311D10	TA311D10	TA311D10	757	8.6	47.8	50	9	AM102745	AM102745	AM102745
685	8.6	47.8	38	10	BE285987	BE285987	601097946	758	8.6	47.8	50	9	AM103034	AM103034	AM103034
686	8.6	47.8	38	10	BE310314	BE310314	601087907	759	8.6	47.8	50	9	AM103041	AM103041	AM103041
687	8.6	47.8	38	17	A2592430	A2592430	1M0403B22	760	8.6	47.8	50	9	AM103606	AM103606	AM103606
688	8.6	47.8	38	17	A2785597	A2785597	2M0029C08	761	8.6	47.8	50	9	AM103608	AM103608	AM103608
689	8.6	47.8	39	9	AL784237	AL784237	AL784237	762	8.6	47.8	50	9	AM103612	AM103612	AM103612
690	8.6	47.8	39	9	AU254920	AU254920	AU254920	763	8.6	47.8	50	9	AM103660	AM103660	AM103660
691	8.6	47.8	39	12	BE788284	BE788284	602114017	764	8.6	47.8	50	9	AM103882	AM103882	AM103882
692	8.6	47.8	39	12	BG819250	BG819250	602781407	765	8.6	47.8	50	9	AM103886	AM103886	AM103886
693	8.6	47.8	39	14	H57425	H57425	y13811.s1	766	8.6	47.8	50	9	AM104152	AM104152	AM104152
694	8.6	47.8	39	17	A2776938	A2776938	2M0011F03	767	8.6	47.8	50	9	AM104160	AM104160	AM104160
695	8.6	47.8	39	17	CNS07GXQ	CNS07GXQ	AA610352	768	8.6	47.8	50	9	AM104232	AM104232	AM104232
696	8.6	47.8	40	9	AA468566	AA468566	ne07e04.s	769	8.6	47.8	50	9	AM104403	AM104403	AM104403
697	8.6	47.8	40	13	B1544620	B1544620	603242263	770	8.6	47.8	50	9	AM104405	AM104405	AM104405
698	8.6	47.8	40	17	A2796990	A2796990	2M0052P23	771	8.6	47.8	50	9	AM104687	AM104687	AM104687
699	8.6	47.8	40	17	BH865895	BH865895	SALK.1000	772	8.6	47.8	50	9	AM104723	AM104723	AM104723
700	8.6	47.8	41	13	B1828498	B1828498	603078276	773	8.6	47.8	50	9	AM104726	AM104726	AM104726
701	8.6	47.8	41	17	A2480375	A2480375	1M0301A20	774	8.6	47.8	50	9	AM104733	AM104733	AM104733
702	8.6	47.8	41	17	A2785555	A2785555	2M0029G04	775	8.6	47.8	50	9	AM104738	AM104738	AM104738
703	8.6	47.8	42	9	AL585489	AL585489	AL585489	776	8.6	47.8	50	9	AM104778	AM104778	AM104778
704	8.6	47.8	42	13	B1223563	B1223563	602941991	777	8.6	47.8	50	9	AM105421	AM105421	AM105421
705	8.6	47.8	42	13	B1665361	B1665361	603288893	778	8.6	47.8	50	9	AM105499	AM105499	AM105499
706	8.6	47.8	42	17	A2309443	A2309443	1M0013011	779	8.6	47.8	50	9	AM105500	AM105500	AM105500
707	8.6	47.8	42	17	A2329441	A2329441	1M0053M07	780	8.6	47.8	50	9	AM105503	AM105503	AM105503
708	8.6	47.8	42	17	A2586799	A2586799	1M0394F04	781	8.6	47.8	50	9	AM105725	AM105725	AM105725
709	8.6	47.8	42	17	BH627368	BH627368	100707D00	782	8.6	47.8	50	9	AM105793	AM105793	AM105793
710	8.6	47.8	43	9	AA932697	AA932697	co074d06.s	783	8.6	47.8	50	9	AM105795	AM105795	AM105795
711	8.6	47.8	43	9	AT036497	AT036497	ub65g12.r	784	8.6	47.8	50	9	AM105800	AM105800	AM105800
712	8.6	47.8	43	9	AT098177	AT098177	ue31a07.x	785	8.6	47.8	50	9	AM105841	AM105841	AM105841
713	8.6	47.8	43	9	AT437739	AT437739	sa39a01.y	786	8.6	47.8	50	9	AM105846	AM105846	AM105846
714	8.6	47.8	43	9	AT186712	AT186712	uj56b03.x	787	8.6	47.8	50	9	AM105847	AM105847	AM105847
715	8.6	47.8	43	9	AT1971753	AT1971753	wr07g07.x	788	8.6	47.8	50	9	AM105901	AM105901	AM105901
716	8.6	47.8	43	9	AA625723	AA625723	ad10f02.s	789	8.6	47.8	50	9	AM106022	AM106022	AM106022
717	8.6	47.8	43	14	H56932	H56932	y07h01.s1	790	8.6	47.8	50	9	AM106282	AM106282	AM106282
718	8.6	47.8	43	17	A2491975	A2491975	1M0325F17	791	8.6	47.8	50	9	AM106292	AM106292	AM106292
719	8.6	47.8	43	17	A2584834	A2584834	1M0389E15	792	8.6	47.8	50	9	AM107600	AM107600	AM107600
720	8.6	47.8	43	17	A2799781	A2799781	2M0057K23	793	8.6	47.8	50	9	AM107631	AM107631	AM107631
721	8.6	47.8	44	9	AL449735	AL449735	AL449735	794	8.6	47.8	50	9	AM107632	AM107632	AM107632
722	8.6	47.8	44	17	A2760710	A2760710	1M0554F08	795	8.6	47.8	50	9	AM107929	AM107929	AM107929
723	8.6	47.8	44	17	AL760705	AL760705	Arabidops	796	8.6	47.8	50	9	AM108013	AM108013	AM108013
724	8.6	47.8	45	10	AV950473	AV950473	AV950473	797	8.6	47.8	50	9	AM255145	AM255145	AM255145
725	8.6	47.8	45	12	BG772081	BG772081	602721525	798	8.6	47.8	50	10	AM768769	AM768769	AM768769
726	8.6	47.8	45	17	BH791506	BH791506	SALK_0600	799	8.6	47.8	50	14	D18207	D18207	MUSGS00477
727	8.6	47.8	46	9	AA703753	AA703753	ag78b06.r	800	8.6	47.8	50	17	UA4315	UA4315	EUW44315.As
728	8.6	47.8	46	9	AA722219	AA722219	zh21a09.s	801	8.6	47.8	50	17	T4215A01P	T4215A01P	EUW43508.T.brucel
729	8.6	47.8	46	9	AT019594	AT019594	ua91a06.r	802	8.6	47.8	50	16	AT582256	AT582256	tg65f03.x
730	8.6	47.8	46	9	AT667606	AT667606	fd16e11.x	803	8.6	47.8	19	17	A2481973	A2481973	1M0306C12
731	8.6	47.8	46	9	AT1701058	AT1701058	wc78c06.x	804	8.6	47.8	19	17	A2761740	A2761740	1M0556A13
732	8.6	47.8	46	9	AT1794993	AT1794993	sb74g08.y	805	8.6	47.8	20	17	A2823352	A2823352	2M0097A22
733	8.6	47.8	46	9	AT1894320	AT1894320	mt69a11.x	806	8.6	47.8	20	17	A2853501	A2853501	2M0156A18
734	8.6	47.8	46	9	AA604908	AA604908	no85d08.s	807	8.6	47.8	22	9	AT444134	AT444134	fb44a01.y
735	8.6	47.8	46	14	R72281	R72281	y189a08.s1	808	8.6	47.8	22	17	A2437792	A2437792	1M0226P14
736	8.6	47.8	46	17	A2325750	A2325750	1M0048H21	809	8.6	47.8	22	17	A2795491	A2795491	2M0049E15

C 810	8.4	46.7	23	17	A2655495	A265495	1M0530E20	883	8.4	46.7	38	12	BF121322	BF121322	601759481
811	8.4	46.7	25		AA917443	AA917443	0151d05.s	884	8.4	46.7	38	12	BF137365	BF137365	601780736
812	8.4	46.7	25		AA93070	AA93070	ou01e06.s	885	8.4	46.7	38	12	BF141985	BF141985	1M0196704
813	8.4	46.7	25	17	A1539187	A1539187	tp78h07.x	886	8.4	46.7	38	17	A2447531	A2447531	1M0244C15
C 814	8.4	46.7	25	17	A2335392	A2335392	1M0065M18	887	8.4	46.7	38	17	A2500985	A2500985	1M0339F07
C 815	8.4	46.7	27	17	A2308445	A2308445	1M0011J22	888	8.4	46.7	38	17	A2816996	A2816996	2M0086B01
C 816	8.4	46.7	27	17	A2966603	A2966603	2M0237J12	889	8.4	46.7	39	14	C02222	C02222	HUGS000656
817	8.4	46.7	28	9	AA905471	AA905471	ok01f11.s	C 890	8.4	46.7	39	17	A2828829	A2828829	2M0106C05
C 818	8.4	46.7	28	9	A1790546	A1790546	u102e08.x	891	8.4	46.7	40	9	AA989688	AA989688	u48811.r
C 819	8.4	46.7	28	17	A2444108	A2444108	1M0239J10	892	8.4	46.7	40	9	A1288030	A1288030	qu99e04.x
C 820	8.4	46.7	28	17	A2782045	A2782045	2M0021N19	893	8.4	46.7	40	13	BF1821604	BF1821604	603036637
C 821	8.4	46.7	29	17	A2985140	A2985140	2M0256H20	C 894	8.4	46.7	40	17	BH801678	BH801678	1008119C0
C 822	8.4	46.7	29	17	A2994186	A2994186	2M0279K01	895	8.4	46.7	40	17	BH804535	BH804535	1008102H0
823	8.4	46.7	30	10	AV833957	AV833957	AV833957	896	8.4	46.7	40	17	BF168070	BF168070	1.1.DUCE1
824	8.4	46.7	30	17	A2339917	A2339917	1M0071B08	897	8.4	46.7	41	13	BF1659995	BF1659995	603302286
C 825	8.4	46.7	30	17	A2344681	A2344681	2M0205K09	C 898	8.4	46.7	41	13	BF160663	BF160663	603044847
C 826	8.4	46.7	31	9	AA678305	AA678305	Arabi1d0ps	C 899	8.4	46.7	41	14	RS5401	RS5401	yq22a03.s1
C 827	8.4	46.7	31	9	AA962313	AA962313	z116b03.s	C 900	8.4	46.7	41	17	A2662545	A2662545	1M0541P07
C 828	8.4	46.7	31	9	A1021071	A1021071	oa99f05.r	C 901	8.4	46.7	42	13	BF1388662	BF1388662	EST-CD34N
C 829	8.4	46.7	31	9	A1159929	A1159929	qb67c08.x	C 902	8.4	46.7	42	14	N98859	N98859	z4e8c04.r1
C 830	8.4	46.7	31	9	A1174159	A1174159	vz84e05.r	C 903	8.4	46.7	42	17	A2770484	A2770484	1M0572006
C 831	8.4	46.7	31	9	A1916122	A1916122	w147a09.x	C 904	8.4	46.7	42	17	A2828302	A2828302	2M0105O11
832	8.4	46.7	31	9	AA243105	AA243105	zr25c04.x	C 905	8.4	46.7	43	9	AA948203	AA948203	op99h09.s
833	8.4	46.7	31	10	AV963388	AV963388	u66e07.r	C 906	8.4	46.7	43	9	AA140455	AA140455	me99a05.r
C 834	8.4	46.7	32	9	A1790007	A1790007	u66e07.r	C 907	8.4	46.7	43	9	A1591196	A1591196	tw12e05.x
C 835	8.4	46.7	32	17	A2826678	A2826678	2M0102P06	C 908	8.4	46.7	43	9	A1610262	A1610262	1M14C11.x
836	8.4	46.7	32	17	DR1N11T	DR1N11T	603179513	C 909	8.4	46.7	43	9	A1625677	A1625677	lv59b11.x
C 838	8.4	46.7	33	13	BF194569	BF194569	603179513	910	8.4	46.7	43	9	A1696963	A1696963	w476c08.x
C 839	8.4	46.7	33	13	BF194569	BF194569	603179513	911	8.4	46.7	43	9	A1780435	A1780435	u101808.x
C 840	8.4	46.7	33	17	A2595031	A2595031	1M0531B23	C 912	8.4	46.7	43	13	BF160624	BF160624	603320073
841	8.4	46.7	33	17	A2595031	A2595031	1M0531B23	C 913	8.4	46.7	43	17	A2585629	A2585629	1M0350K23
842	8.4	46.7	33	17	A2781627	A2781627	2M0021F10	C 914	8.4	46.7	43	17	A2592859	A2592859	1M0403B17
843	8.4	46.7	33	17	A2821136	A2821136	2M0093G16	C 915	8.4	46.7	43	17	AA883443	AA883443	am25d01.s
844	8.4	46.7	33	17	A1722821	A1722821	fc32a11.y	C 916	8.4	46.7	44	12	BG393387	BG393387	602411730
C 845	8.4	46.7	34	9	A1738615	A1738615	w111b02.x	C 917	8.4	46.7	44	13	BF131132	BF131132	602411730
C 846	8.4	46.7	34	12	BG419947	BG419947	602453619	C 918	8.4	46.7	44	17	A2812365	A2812365	2M0079D02
C 847	8.4	46.7	34	13	BF160415	BF160415	603045424	C 919	8.4	46.7	44	17	A2812365	A2812365	2M0079D02
C 848	8.4	46.7	34	13	BF183379	BF183379	603088549	C 920	8.4	46.7	45	17	BH805307	BH805307	1M008066B0
C 849	8.4	46.7	34	13	BF1872725	BF1872725	603397264	C 921	8.4	46.7	45	17	A2602117	A2602117	1M0420P11
C 850	8.4	46.7	34	17	AC073368	AC073368	EP(2)2174	C 922	8.4	46.7	45	17	A2653181	A2653181	1M0526B14
C 851	8.4	46.7	34	17	AC073608	AC073608	EP(2)2462	C 923	8.4	46.7	45	17	A2945177	A2945177	2M0206P23
C 852	8.4	46.7	34	17	AC073734	AC073734	EP(2)2621	C 924	8.4	46.7	45	17	BH846671	BH846671	SAIK-0096
C 853	8.4	46.7	34	17	A2428996	A2428996	1M0212C07	C 925	8.4	46.7	45	17	TA309B10Q	TA309B10Q	
854	8.4	46.7	34	17	A2785014	A2785014	2M0028D03	C 926	8.4	46.7	46	9	AA658179	AA658179	v196b01.r
C 855	8.4	46.7	34	17	TA125E10P	TA125E10P		C 927	8.4	46.7	46	9	AA652871	AA652871	ns75e09.s
C 856	8.4	46.7	35	10	BE531379	BE531379		C 928	8.4	46.7	46	9	AA736376	AA736376	z977a12.s
C 857	8.4	46.7	35	13	BF1907298	BF1907298	603063892	C 929	8.4	46.7	46	9	AA929076	AA929076	om77f07.s
858	8.4	46.7	35	17	A2623189	A2623189	1M0460F05	C 930	8.4	46.7	46	9	A1544740	A1544740	qf72d04.x
859	8.4	46.7	35	17	A2820699	A2820699	2M0093L02	C 931	8.4	46.7	46	9	A1690532	A1690532	lq12e07.x
860	8.4	46.7	35	17	DR10P1T	DR10P1T		C 932	8.4	46.7	46	9	AA238784	AA238784	mx82h02.r
861	8.4	46.7	36	12	BF347689	BF347689	Dm10.rct	C 933	8.4	46.7	46	9	AA433800	AA433800	v156l06.r
862	8.4	46.7	36	12	A2467565	A2467565	602022291	C 934	8.4	46.7	46	9	AA480238	AA480238	vi36l06.r
C 863	8.4	46.7	37	9	AA932304	AA932304	om37908.s	C 935	8.4	46.7	46	10	AAV833431	AAV833431	AV833431
C 864	8.4	46.7	37	9	A1089361	A1089361	qb05h05.x	C 936	8.4	46.7	46	14	N78054	N78054	yv17g05.r1
C 865	8.4	46.7	37	9	A1194600	A1194600	ue65a09.r	C 937	8.4	46.7	46	17	A2449175	A2449175	1M0247K13
866	8.4	46.7	37	9	A1719694	A1719694	as58b05.x	C 938	8.4	46.7	46	17	A2595176	A2595176	1M0407D12
867	8.4	46.7	37	9	A1721631	A1721631	fc30c09.x	C 939	8.4	46.7	46	17	A2663583	A2663583	1M0543J13
868	8.4	46.7	37	10	AA949641	AA949641		C 940	8.4	46.7	46	17	BH851050	BH851050	SAIK-0723
869	8.4	46.7	37	10	BE407487	BE407487	601300314	C 941	8.4	46.7	47	9	AA290779	AA290779	zr22g02.r
C 870	8.4	46.7	37	12	BC393320	BC393320	602411536	C 942	8.4	46.7	47	13	BF156866	BF156866	602921488
C 871	8.4	46.7	37	14	N90070	N90070	2b23b04.s1	C 943	8.4	46.7	47	13	BF160112	BF160112	603044604
C 872	8.4	46.7	37	17	A2595066	A2595066	1M0407M22	C 944	8.4	46.7	47	13	BF160112	BF160112	603044604
C 873	8.4	46.7	37	17	A2824274	A2824274	2M0098I15	C 945	8.4	46.7	48	12	BF035895	BF035895	601457806
C 874	8.4	46.7	37	17	A2827794	A2827794	2M0104L22	C 946	8.4	46.7	48	12	BF035895	BF035895	601457806
C 875	8.4	46.7	37	17	A2828221	A2828221	2M0105P03	C 947	8.4	46.7	48	17	A2476171	A2476171	1M0294D13
C 876	8.4	46.7	37	17	A2867587	A2867587	2M0178B06	C 948	8.4	46.7	48	17	A2629734	A2629734	1M0482K19
C 877	8.4	46.7	37	17	BH757562	BH757562	SAIK_0565	C 949	8.4	46.7	48	17	A2767769	A2767769	1M0567H13
C 878	8.4	46.7	37	17	A1768567	A1768567	Arabi1d0ps	C 950	8.4	46.7	48	17	A2794791	A2794791	2M0048B13
C 879	8.4	46.7	38	9	AL681254	AL681254	Arabi1d0ps	C 951	8.4	46.7	48	17	BH797135	BH797135	100808B61
C 880	8.4	46.7	38	10	BE261178	BE261178	601125951	C 952	8.4	46.7	48	17	BH897484	BH897484	3520.r1-B-
881	8.4	46.7	38	10	BE285987	BE285987	601097946	C 953	8.4	46.7	49	9	AA013617	AA013617	mm10d05.r
882	8.4	46.7	38	10	BE310314	BE310314	601087907	C 954	8.4	46.7	49	9	AA948394	AA948394	on52b09.s
								C 955	8.4	46.7	49	9	A1445610	A1445610	l308a02.x

C 956	8.4	46.7	49	9	AA4500193
C 957	8.4	46.7	49	9	AA452723
C 958	8.4	46.7	49	12	BF722018
C 959	8.4	46.7	49	12	BF342803
C 960	8.4	46.7	49	13	BI873153
C 961	8.4	46.7	49	13	BI873153
C 962	8.4	46.7	49	13	BI030790
C 963	8.4	46.7	49	14	R53501
C 964	8.4	46.7	49	14	R54986
C 965	8.4	46.7	49	17	A2472469
C 966	8.4	46.7	49	17	A2475365
C 967	8.4	46.7	49	17	A2788840
C 968	8.4	46.7	49	17	A2830102
C 969	8.4	46.7	49	17	BH855632
C 970	8.4	46.7	50	9	AA076000
C 971	8.4	46.7	50	9	AA076000
C 972	8.4	46.7	50	9	AA076000
C 973	8.4	46.7	50	9	AA076000
C 974	8.4	46.7	50	9	AA076000
C 975	8.4	46.7	50	9	AA076000
C 976	8.4	46.7	50	9	AA076000
C 977	8.4	46.7	50	9	AA076000
C 978	8.4	46.7	50	9	AA076000
C 979	8.4	46.7	50	9	AA076000
C 980	8.4	46.7	50	9	AA076000
C 981	8.4	46.7	50	9	AA076000
C 982	8.4	46.7	50	9	AA076000
C 983	8.4	46.7	50	9	AA076000
C 984	8.4	46.7	50	9	AA076000
C 985	8.4	46.7	50	9	AA076000
C 986	8.4	46.7	50	9	AA076000
C 987	8.4	46.7	50	9	AA076000
C 988	8.4	46.7	50	9	AA076000
C 989	8.4	46.7	50	9	AA076000
C 990	8.4	46.7	50	9	AA076000
C 991	8.4	46.7	50	9	AA076000
C 992	8.4	46.7	50	9	AA076000
C 993	8.4	46.7	50	9	AA076000
C 994	8.4	46.7	50	9	AA076000
C 995	8.4	46.7	50	9	AA076000
C 996	8.4	46.7	50	9	AA076000
C 997	8.4	46.7	50	9	AA076000
C 998	8.4	46.7	50	9	AA076000
C 999	8.4	46.7	50	9	AA076000
C 1000	8.4	46.7	50	9	AA076000

ALIGNMENTS

[illegible]

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouse@stwatson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:980209
Trace considered overall poor quality
Possible reversed clone; similarity on wrong strand
Seq primer: custom primer used
High quality sequence stop: 1.
Location/Qualifiers
1..43

```

/clone-"IMAGE:1923917"
/clone_1lb="Sugano mouse liver mila"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
(CACCTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dt) primer
[ATGTGGCCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTGGCCCTCATGTG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACCTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTGTGCTCTTAAGAATGCG and 3' end
primer CGACCTGCGACCTGACACAC.

```

Query Match	74.4%	Score	13.4	DB	9	Length	43
Best Local Similarity	93.3%	Pred. NO.	1.9e+04				
Matches	14	Conservative	0	Mismatches	1	Indels	0
				Gaps			0

Qy	1	CCCGAAGGCAGTCT	15
Db	17	CAACGGAAGGCAGTCT	31

RESULT 2	AA11398/c	LOCUS	DEFINITION
AA11398	40 bp	mRNA	linear
mp10f06.c1	Life Tech mouse embryo	8 5dpc	10664019 Mus musculus cDNA
clone IMAGE:568835	5'	similar to TR:G881558	G881558 PHAS-I. [1] ,
mRNA	SEQUENCE.		

ACCESSION AA111398
 VERSION AA111398.1 GI:1663279
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 40)
 REFERENCE Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubugue, T., Giesel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, B., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, P., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
 TITLE The WashU-HMHI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HMHI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: mouseest@atson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:343483

Possible reversed clone: similarity on wrong strand
Seq primer: -28M13 rev1 from Amerham
High quality sequence stop: 9.

FEATURES

source

1. 40
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_id="Life Tech mouse embryo 8 5dpc 10664019"
/tissue_type="embryo"
/dev_stage="8.5dpc embryos"
/lab_host="DH10B"
/note="Organ: whole embryo; Vector: pCMV-SPORT2; Site:1;
Salt: Site:2: NotI; Cloned unidirectionally. Primer:
Oligo dt. 8.5dpc embryos. pCMV-SPORT2 vector."
BASE COUNT 6 a 16 c 15 g 3 t
ORIGIN

Query Match 73.3%; Score 13.2; DB 9; Length 40;
Best Local Similarity 83.3%; Pred. No. 2.3e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CCGGAGGAGCGACTGTGGC 18
||||| |||||||
Db 38 CCGGCTGGGAGACTGTGGC 21

RESULT 3
LOCUS B1246232 36 bp mRNA linear EST 17-JUL-2001
DEFINITION B1246232.1 NCL CGAP_L19 Mus musculus cDNA clone IMAGE:5124378 5',
mRNA sequence.
ACCESSION B1246232.1 GI:14789788
VERSION B1246232.1
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey F. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: L19M1304 row: a column: 19
High quality sequence stop: 36.
Location/Qualifiers

1. 36
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_id="IMAGE:5124378"
/clone_id="NCL CGAP_L19"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site:1: NotI;
Site:2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCL CGAP Library."
BASE COUNT 7 a 8 c 17 g 4 t
ORIGIN

FEATURES

source

1. 36
Location/Qualifiers
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_id="IMAGE:5124378"
/clone_id="NCL CGAP_L19"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site:1: NotI;
Site:2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCL CGAP Library."
BASE COUNT 7 a 8 c 17 g 4 t
ORIGIN

Query Match 67.8%; Score 12.2; DB 13; Length 36;
Best Local Similarity 82.4%; Pred. No. 6.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CCGGAGGAGCGACTGTGG 17
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Db 4 CCGGAGGAGCGACTGTGG 20

RESULT 4
LOCUS AU104269 50 bp mRNA linear EST 30-AUG-2001
DEFINITION AU104269 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ZRV61769, mRNA sequence.
ACCESSION AU104269
VERSION AU104269.1 GI:13553790
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers

1. 50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="ZRV61769"
/clone_id="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfumarate treated U937 cells"
BASE COUNT 12 a 15 c 14 g 7 t 2 others
ORIGIN

Query Match 67.8%; Score 12.2; DB 9; Length 50;
Best Local Similarity 82.4%; Pred. No. 7.2e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CCGGAGGAGCGACTGTGG 17
||||| |||||||
Db 9 CCGGAGGAGCGACTGTGG 25

RESULT 5
LOCUS A2824475 30 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0099001F Mouse 10kb plasmid UGCC1M library Mus musculus genomic
clone UGCC2M0099001 F, DNA sequence.
ACCESSION A2824475
VERSION A2824475.1 GI:12994383
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 30)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellily

1 (bases 1 to 30)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellily

TITLE
JOURNAL
COMMENT
, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10Kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0099 row: 0 column: 01
Seq primer: CTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers

FEATURES
SOURCE

1. 30
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0099001"
/clone_lib="Mouse 10Kb plasmid UUCG1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/shares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of Plasmid RI, the vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT
ORIGIN

6 a 11 c 6 g 7 t

Query Match 65.6%; Score 11.8; DB 17; Length 30;
Best Local Similarity 86.7%; Pred. No. 1e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CCCGGAAGCAGCTT 15
11 |||||||
Db 11 CCTGGAAGTCACTT 25

RESULT 6
AA975650/c 42 bp mRNA linear EST 22-MAY-1998
LOCUS oq3d09.s1 NCI_CGAP_Kid6 Homo sapiens cDNA IMAGE:1591025 3'
DEFINITION similar to gb:M71172.cdsl ZINC FINGER PROTEIN 22 (HUMAN);, mRNA
sequence.
ACCESSION AA975650
VERSION AA975650.1 GI:3151442
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 42)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE
JOURNAL
COMMENT
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/BLND at:
www.bio.linnl.gov/bbrp/image/image.html
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers

FEATURES
SOURCE

1. 42
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1591025"
/clone_lib="NCI_CGAP_Kid6"
/sex="mixed"
/tissue_type="kidney tumor"
/lab_host="SQR (kanamycin resistant)"
/note="Organ: kidney; Vector: Bluescript SK-; Site_1:
EcorI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Pooled kidney tumors. 5' adaptor sequence: 5'
GAATTCGGCAGAG 3' 3' adaptor sequence: 5'
CTCAGCTTTTTTTTTTTTTTTT 3' Average insert size: 1.0 kb."
BASE COUNT 10 a 16 c 7 g 9 t

BASE COUNT
ORIGIN

Query Match 65.6%; Score 11.8; DB 9; Length 42;
Best Local Similarity 86.7%; Pred. No. 1e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CCGGAAGCAGTCTG 16
1 |||||||
Db 29 CAGGAAGCAAGTCTG 15

RESULT 7
A2815319 45 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0083A05R Mouse 10Kb plasmid UUCG1M library Mus musculus genomic
DEFINITION clone UUCG2M0083A05 R, DNA sequence.
ACCESSION A2815319
VERSION A2815319.1 GI:12985227
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 45)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Kelly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10Kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0083 row: A column: 05
Seq primer: CACACGAAACAGCTATGACC
Class: plasmid ends

FEATURES

source

High quality sequence stop: 45.

Location/Qualifiers

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1. .45
/organism="Mus musculus"
/strain="C57BL/6J"
/db.xref="taxon:10090"
/clone="U9C2M0083A05"
/clone.lib="mouse 10kb plasmid U9C1M library"
/sex="male"
/lab.host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD42ny. Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g1147321141p/AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

BASE COUNT 5 a 14 c 12 g 14 t

ORIGIN

Query Match 65.6%; Score 11.8; DB 17; Length 45;
Best Local Similarity 86.7%; Pred. No. 1.1e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 GGAGGAGCTGTGGC 18
1111 1111 1111
Db 30 GGATGCACTTGGC 44

RESULT 8

BI252223/c 42 bp mRNA linear EST 17-JUL-2001

LOCUS 602953127F1 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:5087239 5',

DEFINITION mRNA sequence.

ACCESSION BI252223.1 GI:14802469

VERSION EST.

KEYWORDS human.

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 42)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: CGAP (Stanford)

cDNA Library Preparation: Ling Hong/Rubin Laboratory

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov f column: 08

Plate: L10CMI844 row: f column: 08

High quality sequence stop: 42.

Location/Qualifiers

1. .42

/organism="Homo sapiens"

/db.xref="taxon:9606"

/clone="IMAGE:5087239"

FEATURES

source

/clone.lib="NIH_MGC_100"

/tissue_type="hepatocellular carcinoma, cell line"

/lab.host="DH10B (phage-resistant)"

/note="Organ: Liver; Vector: pORF7. Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dt priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGGCGGCGG(C). Size-selected by 500bp for average insert size

1.8kb. Library constructed by Ling Hong in the Laboratory

of Gerald M. Rubin (University of California, Berkeley)

using ZAP-cDNA synthesis kit (Stratagene) and Superscript

II RT (Life Technologies). Note: this is a NIH-MGC

Library."

BASE COUNT 4 a 20 c 13 g 5 t

ORIGIN

Query Match 64.4%; Score 11.6; DB 13; Length 42;

Best Local Similarity 77.8%; Pred. No. 1.3e+05;

Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CCCGGAGGAGCTGTGGC 18

1111 1111 1111

Db 23 CCCGGAGGAGCTGTGGC 6

RESULT 9

BI252484/c 42 bp mRNA linear EST 17-JUL-2001

LOCUS 602952948F1 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:5087458 5',

DEFINITION mRNA sequence.

ACCESSION BI252484.1 GI:14802986

VERSION EST.

KEYWORDS human.

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 42)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: CGAP (Stanford)

cDNA Library Preparation: Ling Hong/Rubin Laboratory

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov f column: 11

Plate: L10CMI844 row: o column: 11

High quality sequence stop: 42.

Location/Qualifiers

1. .42

/organism="Homo sapiens"

/db.xref="taxon:9606"

/clone="IMAGE:5087458"

/clone.lib="NIH_MGC_100"

/tissue_type="hepatocellular carcinoma, cell line"

/note="Organ: Liver; Vector: pORF7. Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dt priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGGCGGCGG(C). Size-selected by 500bp for average insert size

1.8kb. Library constructed by Ling Hong in the Laboratory

of Gerald M. Rubin (University of California, Berkeley)

using ZAP-cDNA synthesis kit (Stratagene) and Superscript

II RT (Life Technologies). Note: this is a NIH-MGC

BASE COUNT 4 a 20 c 13 g 5 t

ORIGIN

Query Match 64.4%; Score 11.6; DB 13; Length 42;

Best Local Similarity 77.8%; Pred. No. 1.3e+05;

Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CCCGGAGGAGCTGTGGC 18

1111 1111 1111

Db 23 CCCGGAGGAGCTGTGGC 6

RESULT 9

BI252484/c 42 bp mRNA linear EST 17-JUL-2001

LOCUS 602952948F1 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:5087458 5',

DEFINITION mRNA sequence.

Matches 14: Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 CCCGAGGAGCTGTGGC 18
||||| ||||| |||
Db 23 CCCGCGGCGCACTGCGGC 6

RESULT 10
CNS07HVN/C
LOCUS
DEFINITION CNS07HVN 45 bp DNA linear GSS 03-OCT-2001
Anopheles gambiae GSS 77 end of clone 30P21 of library Notredame1
from strain PEST of Anopheles gambiae (African malaria mosquito),
genomic survey sequence.

ACCESSION
VERSION AL611573
KEYWORDS
SOURCE African malaria mosquito.

ORGANISM
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Anopheles.

REFERENCE
TITLES 1 (bases 1 to 45)
Genoscope.
AUTHORS Direct Submission
JOURNAL Submitted (01-OCT-2001) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
Web : www.genoscope.cns.fr

2 (bases 1 to 45)
Roth,C.W., Brey,P.T., Ke,Z. and Collins,F.H.

REFERENCE
AUTHORS Direct Submission
TITLES Submitted (01-OCT-2001) BIKI, Institut Pasteur, 25, rue du Dr.
JOURNAL Roux, Paris 75015, France

COMMENT
This clone is from an A. gambiae BAC library provided by F.H.
Collins and sequenced by Genoscope in collaboration with the
Laboratory of Biochem. and Biol. Molec. of Insects, Institut
Pasteur.

FEATURES
source
1. .45
/organism="Anopheles gambiae"
/strain="PEST"
/db_xref="taxon:7165"
/clone="30P21"
/clone_lib="Notredame1"
/note="end : 77"

BASE COUNT
ORIGIN 9 a 6 c 12 g 18 t

Query Match 64.4%; Score 11.6; DB 17; Length 45;
Best Local Similarity 77.8%; Pred. No. 1.4e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 CCCGAGGAGCTGTGGC 18
||||| ||||| |||
Db 44 CCCATAGTCAGTCCGCGC 27

RESULT 11
AU102427/C
LOCUS
DEFINITION AU102427 50 bp mRNA linear EST 30-AUG-2001
Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ADA002325, mRNA sequence.

ACCESSION
VERSION AU102427
KEYWORDS
SOURCE human.

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale

TITLE

JOURNAL
MEDLINE
21270072
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source
1. .50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ADA002325"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfluminate treated u937 cells"

BASE COUNT
ORIGIN 5 a 15 c 18 g 12 t

Query Match 64.4%; Score 11.6; DB 9; Length 50;
Best Local Similarity 77.8%; Pred. No. 1.4e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 CCCGAGGAGCTGTGGC 18
||||| ||||| |||
Db 28 CCAGGAGCGAGCTGTCTC 11

RESULT 12
AU102430/C
LOCUS
DEFINITION AU102430 50 bp mRNA linear EST 30-AUG-2001
Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ADS001588, mRNA sequence.

ACCESSION
VERSION AU102430
KEYWORDS
SOURCE human.

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites

TITLE
JOURNAL
MEDLINE
21270072
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source
1. .50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ADS001588"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfluminate treated u937 cells"

BASE COUNT
ORIGIN 5 a 15 c 18 g 12 t

Query Match 64.4%; Score 11.6; DB 9; Length 50;
Best Local Similarity 77.8%; Pred. No. 1.4e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCCGAGGACGACTGCGC 18
 Db 30 CCGAGACGACGAGCTGTC 13

RESULT 13
 AUI02431/C 50 bp mRNA linear EST 30-AUG-2001
 LOCUS AUI02431 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 DEFINITION AUI02431 mRNA sequence.
 ACCESSION AUI02431
 VERSION AUI02431.1 GI:13551951
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 50)
 AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
 ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
 ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
 Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites
 EMBO Rep. 2 (5), 388-393 (2001)
 21270072
 COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yutaka@ims.u-tokyo.ac.jp
 Suzuki,Y., Toshitomo Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
 ,S. Construction and characterization of a full length-enriched and
 a 5'-end enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
 Location/Qualifiers
 1..50
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="ADS01912"
 /clone_1lb="Sugano Homo sapiens cDNA library"
 /note="Differential display comparison of untreated and
 dimethylfumarate treated U937 cells"
 16 c 18 g 9 t

BASE COUNT 7 a 16 c 18 g 9 t
 ORIGIN

Query Match 64.4% Score 11.6; DB 9; Length 50;
 Best Local Similarity 77.8%; Pred. No. 1.4e+05;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCCGAGGACGACTGCGC 18
 Db 36 CCGAGACGACGAGCTGTC 19

RESULT 14
 A2821049 22 bp DNA linear GSS 20-FEB-2001
 LOCUS A2821049 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC2M0093G07 R, DNA sequence.
 ACCESSION A2821049
 VERSION A2821049.1 GI:12990957
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 22)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C.,
 Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly
 ,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SIC, UT
 84112 USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dduenne@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0093 row: 6 column: 07
 Seq primer: CACACAGGAACGACTATGACC
 Class: plasmid ends
 High quality sequence stop: 22.
 Location/Qualifiers
 1..22
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0093G07"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42ny: Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (g1147321149b|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 3 a 8 c 8 g 3 t
 ORIGIN

Query Match 63.2% Score 11.2; DB 17; Length 22;
 Best Local Similarity 81.2%; Pred. No. 1.9e+05;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCGAGGACGACTGTC 16
 Db 17 CCGGAGACGACGCCG 2

RESULT 15
 A2776661 25 bp DNA linear GSS 16-FEB-2001
 LOCUS A2776661 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC2M0010C05 R, DNA sequence.
 ACCESSION A2776661
 VERSION A2776661.1 GI:12904460
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 25)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C.,
 Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly
 ,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

[illegible]

FEATURES	COMMENT
SOURCE	21270072 Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: yusuzuki@ims.u-tokyo.ac.jp Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997). Location/Qualifiers 1..50 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="HEP18127" /clone_1lb="Sugano Homo sapiens cDNA library" /note="Differential display comparison of untreated and dimethylfumarate treated U937 cells"
BASE COUNT	6 a 13 c 18 g 13 t
ORIGIN	
Query Match	62.2%; Score 11.2; DB 9; Length 50;
Best Local Similarity	81.2%; Pred. No. 2.1e+05;
Matches 13; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
QY	3 CGGAGGCACTCTGGC 18
Db	37 CGGAGTCATCGCTG 22
RESULT 17	
LOCUS	50 bp mRNA linear EST 30-AUG-2001
LOCUS	AU104249
DEFINITION	Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP18419, mRNA sequence.	
ACCESSION	AU104249
VERSION	AU104249.1 GI:13553770
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
Chordata; Craniata; Vertebrata; Euteleostomi;	
Eukaryota; Metazoa; Primates; Catarrhini; Homnidae; Homo.	
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
1 (bases 1 to 50)	
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata	
, H., Ota, T., Iisoga, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki	
, Y., Nakamura, Y., Suyama, A. and Sugano, S.	
Diverse transcriptional initiation revealed by fine, large-scale	
mapping of mRNA start sites	
EMBO Rep. 2 (5), 388-393 (2001)	
21270072	
CONTACT: Yutaka Suzuki	
Department of Virology	
Institute of Medical Science, University of Tokyo	
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan	
Email: yusuzuki@ims.u-tokyo.ac.jp	
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano	
, S. Construction and characterization of a full length-enriched and	
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).	
Location/Qualifiers	
1..50	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="HEP18419"	
/clone_1lb="Sugano Homo sapiens cDNA library"	
/note="Differential display comparison of untreated and	
dimethylfumarate treated U937 cells"	
BASE COUNT	12 a 16 c 13 g 9 t
ORIGIN	
Query Match	62.2%; Score 11.2; DB 9; Length 50;
Best Local Similarity	81.2%; Pred. No. 2.1e+05;
Matches 13; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
QY	1 CCGGAGGCACTCTG 16

University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunne@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0275 row: 1 column: 19
 Seq primer: CGTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 42.

FEATURES

source

1. .42
 Location/Qualifiers
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="U08C2M0275I19"
 /clone_1lb="Mouse 10kb plasmid U08C2M 1library"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114|gbl|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
 ORIGIN

9 a 15 c 12 g 6 t

Query Match 60.0%; Score 10.8; DB 17; Length 42;
 Best Local Similarity 85.7%; Pred. No. 3.2e+05;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GGAAGGAGCTCTGG 17
 ||||||| |||||

Db 37 GGCAGGACGCTCG 24

RESULT 21

AL771267

LOCUS AL771267 43 bp DNA linear GSS 19-JUN-2002
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-178G11-013562,
 genomic survey sequence.

ACCESSION

AL771267

VERSION

AL771267.1

KEYWORDS

GSS.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

2

AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

COMMENT

Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weissshaar, B.
 A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
 for flanking sequence tag based reverse genetics
 Unpublished
 3 (bases 1 to 43)
 Li, Y., Rosso, M., Strizhov, N. and Weissshaar, B.
 Direct Submission
 Submitted (17-JUN-2002) Weissshaar B., Max-Planck-Institut fuer
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 This sequence is recovered from the left border of the T-DNA. It
 indicates an insertion close to or within gene At4g03970. The
 sequences are generated at the MPI for Plant Breeding Research in
 the context of the GABI-Kat project. GABI-Kat is part of the German
 Plant Genomics program designated 'GABI'. Information on line
 availability can be found at:
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES

source

1. .43
 Location/Qualifiers
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="GK-178G11-013562"
 /clone_1lb="Arabidopsis thaliana T-DNA insertion lines"
 /note="PCR was performed on DNA from Arabidopsis thaliana
 plants (T1) which were transformed with the T-DNA from
 vector PAC161. The lines contain one or more T-DNA
 insertions. The DNA fragment(s) resulting from the PCR
 were directly sequenced to determine the genomic sequence
 flanking the insertion. Sequences displaying significant
 similarity to the A. thaliana nuclear genome sequence were
 processed for submission. T-DNA derived sequences were
 removed"

BASE COUNT
 ORIGIN

11 a 11 c 10 g 11 t

Query Match 60.0%; Score 10.8; DB 17; Length 43;
 Best Local Similarity 85.7%; Pred. No. 3.2e+05;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCGAAGGAGCTCT 15
 ||||||| |||||

Db 2 CCGAAGCTCAGTCT 15

RESULT 22

W05609/c

LOCUS

DEFINITION

ACCESSION

W05609

VERSION

W05609.1

KEYWORDS

EST.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

W05609 46 bp mRNA linear EST 23-APR-1996
 za85f01.r1 Soares_fetal_lung_NbH19w Homo sapiens cDNA clone
 IMAGE:299353 5' similar to SW:GSH2_RAT P46413 GLUTATHIONE
 SYNTHETASE ; mRNA sequence.
 W05609
 W05609.1 GI:1278320
 EST.
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 46)
 Hillier, L., Clack, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
 M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Matra, M., Parsons, J.,
 Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston
 R., Williamson, A., Wohlmann, P. and Wilson, R.
 The Washu-Merck EST Project
 Unpublished (1995)
 Contact: Wilson RK
 Washington University School of Medicine
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 This clone is available royalty-free through LNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality

[illegible]

RESULT	26
AZ610133/C	
LOCUS	AZ610133 29 bp DNA linear GSS 13-DEC-2000
DEFINITION	1M0435F16r Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION	UUGC1M0435F16 F, DNA sequence.
VERSION	AZ610133
KEYWORDS	AZ610133.1 GI:11732323
SOURCE	GSS.
ORGANISM	house mouse. Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 29) Dunn,D., Aoyagi,A., Barber,M., Baecorn,T., Duval,B., Hamll,C., Islam,H., Longacre,S., Mahmoud M., Meenen,E., Pedersen,T., Reilly, M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0435 Row: F Column: 16 Seq primer: CGTGTAAACGACGCCACT Class: plasmid ends High quality sequence stop: 29. Location/Qualifiers 1..29 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGC1M0435F16" /clone_lib="Mouse 10kb plasmid UUGC1M library" /sex="Male" /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMDA2 (GI4732114[gb AF129072.1]) a copy-number inductible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT	4 a 15 c 4 g 6 t
ORIGIN	
Query Match	58.9%; Score 10.6; DB 17; Length 29;
Best Local Similarity	76.5%; Pred. No. 3.8e+05;
Matches 13; Conservative	0; Mismatches 4; Indels 0; Gaps 0;
CCGCGAAGGCAGTCGG 17	
DB 23 CCAGGAAGGGGTATGCG 7	

RESULT 27
LOCUS T62015/C
DEFINITION 31 bp mRNA linear EST 14-FeB-1995
 yb97c06.r1 Strata gene lung (#937210) Homo sapiens cDNA clone
 IMAGE:79114 5' similar to gb:J03600 ARACHIDONATE 5-LIPOXYGENASE
 (HUMAN); mRNA sequence.
ACCESSION T62015
VERSION T62015.1 GI:665258
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 31)
AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chapell, B.,
 Chissole, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins,
 M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Mardis, E., Moore,
 B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
 Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevisan, E.,
 Underwood, K., Wohlmann, P., Waterston, R., Wilson, R., and Marra, M.
 Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)
TITLE 97044478
JOURNAL Contact: Wilson RK
MEDLINE Washington University School of Medicine
COMMENT 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: estel@wustl.edu
 Insert Size: 489
 High quality sequence stops: 18 Source: IMAGE Consortium, LNL. This
 clone is available royalty-free through LNL; contact the IMAGE
 Consortium (info@image.lnl.gov) for further information. Putative
 full length read
 Insert Length: 489 Std Error: 0.00
 Seq primer: M13RPI
 High quality sequence stop: 18.
FEATURES Location/Qualifiers
 source 1..31
 /organism="Homo sapiens"
 /db_xref="GDB:482731"
 /db_xref="taxon:9606"
 /clone="IMAGE:79114"
 /clone_lib="Stratagene Lung (#937210)"
 /sex="male"
 /dev_stage="72 years"
 /lab_host="SOLR cells (kanamycin resistant)"
 /note="Organ: Lung; Vector: pBluescript SK-; Site_1: EcorI
 ; Site_2: XhoI; Cloned unidirectionally. Primer: OLI30
 dr. normal lung. Average insert size: 1.0 kb; Uni-ZAP XR
 Vector: -3' adaptor sequence: 5' GAATTCGGCAGAG 3' -3'
 adaptor sequence: 5' CTCGACGTTTCTTTTCTTTTCTTTT 3'."
BASE COUNT 6 a 11 c 10 g 4 t
ORIGIN
 Query Match 58.9%; Score 10.6; DB 14; Length 31;
 Best Local Similarity 76.5%; Pred. No. 3.8e+05;
 Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Oy 1 CCCGAGGCGAGCTGTG 17
 ||| ||||| |||||
 Db 31 CCGGAGGCGAGCTGTG 15
RESULT 28
LOCUS AZ953906/C
DEFINITION 38 bp DNA linear GSS 27-APR-2001
 2M0219B22F Mouse 10kb plasmid UUCGCM library Mus musculus genomic
 clone UUCG2M0219B22 F, DNA sequence.
ACCESSION AZ953906
VERSION AZ953906.1 GI:13825133

KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 38)
AUTHORS Dunn, P., Aoyagi, A., Barber, M., Beacorn, T., Duvall, B., Hamill, C.,
 Islam, H., Longcore, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellily
 and Wright, D., Weiss, R., Stokes, R., Tingey, A., von Niederhausern, A.,
 M., Rose, M., Rose, R.,
 Mouse whole genome scaffolding with paired end reads from 10kb
 Plasmid Inserts
 Unpublished (2000)
TITLE Contact: Robert B. Weiss
JOURNAL University of Utah
COMMENT Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0219 row: B column: 22
 Seq primer: CGTGTAAACGACGCGCACT
 Class: plasmid ends
 High quality sequence stop: 38.
FEATURES Location/Qualifiers
 source 1..38
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCG2M0219B22"
 /clone_lib="Mouse 10kb plasmid UUCG2M library"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (female) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (9114/3211419b/AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."
BASE COUNT 1 a 13 c 15 g 9 t
ORIGIN
 Query Match 58.9%; Score 10.6; DB 17; Length 38;
 Best Local Similarity 76.5%; Pred. No. 4e+05;
 Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Oy 2 CCGGAGGCGAGCTGTG 18
 ||||| ||||| |||||
 Db 21 CCGGAGGCGAGCTGTG 5
RESULT 29
LOCUS A0939867
DEFINITION 42 bp DNA linear GSS 23-AUG-2000
 humn9513 CTRB Mouse BMC library Mus musculus genomic, DNA sequence.
ACCESSION A0939867
VERSION A0939867.1 GI:9581521
KEYWORDS GSS.

SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 42)
TITLE	Clark,R.M., Marker,P.C. and Kingsley,D.N. A novel candidate gene for mouse and human preaxial polydactyly with altered expression in limbs of Hemimelic extra-toes mutant mice
JOURNAL	Genomics 67 (1), 19-27 (2000)
MEDLINE	20399563
COMMENT	Contact: Kingsley DM Dept. of Developmental Biology and Howard Hughes Medical Institute Stanford University Beckman Center B300-279 Campus Drive, Stanford, CA 94305, USA Fax: 650 725 7739 Email: kingsley@cgm.stanford.edu Mus musculus chromosome 5, Hammetoe (Hm) region, exon-trapped sequence 13 from D5Mit195 to D5Mit44 interval Class: exon-trapped.
FEATURES	Location/Qualifiers 1..42 /organism="Mus musculus" /strain="129" /db_xref="taxon:10090" /clone_lib="CITB Mouse BAC library" /sex="male" 14 c 10 g 10 t 1 others
BASE COUNT	7 a 14 c 10 g 10 t 1 others
ORIGIN	
Query Match	58.9%; Score 10.6; DB 17; Length 42;
Best Local Similarity	76.5%; Pred. NO.4e+05;
Matches 13; Conservative	0; Mismatches 4; Indels 0; Gaps 0.
QY 2	CCGGAAGCAGCTCTGGC 18 11111111111111111111
Db 16	CTGGAATGCTGACTGTGC 32
RESULT 30	
A2770047/c	42 bp DNA linear GSS 16-FEB-2007
LOCUS	A2770047 Mouse 10kb plasmid U06C1M library Mus musculus genomic
DEFINITION	clone U06C1M0571B19 F, DNA sequence.
ACCESSION	A2770047
VERSION	A2770047.1 GI:12890825
KEYWORDS	GSS.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 42) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
TITLE	Unpublished (2000)
JOURNAL	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT, 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0571 row: B column: 19 Seq primer: CGTTGTAAGACGACGCACGT Class: plasmid ends High quality sequence stop: 42. Location/Qualifiers
COMMENT	

source	1. 42	/organism="Mus musculus"
		/strain="C57BL/6J"
		/db_xref="taxon:10090"
		/clone="UUGC1M0571B19"
		/clone_lib="Mouse 10kb plasmid UUGC1M library"
		/sex="Male"
		/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
		/note="Vector: PMD42mv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
		(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g11473211419b/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT	1 a	21 c 10 g 10 t
ORIGIN		
Query Match	58.9%	Score 10.6; DB 17; Length 42;
Best Local Similarity	76.5%	Pred. No. 4e+05;
Matches 13; Conservative	0; Mismatches 4; Indels 0; Gaps 0;	
QY	2 CCGAGAGCGACTCTGGC 18	1 11 11111 1 11
Db	21 CAGCGAGCGAGCGAGGC 5	
RESULT 31		
LOCUS	H63217	43 bp mRNA linear EST 11-OCT-1995
DEFINITION	Y48F07 r1 Soares fetal liver spleen INTLS Homo sapiens CDNA clone IMAGE:208549.5, similar to SP:A6159 A6159 ISGF-3 91 KDA COMPONENT=INTERFERON-DEPENDENT POSITIVE-ACTING TRANSCRIPTION FACTOR(ISGF-3 84 KDA COMPONENT) - ; mRNA sequence.	
ACCESSION	H63217	
VERSION	H63217.1	GI:1018018
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
AUTHORS	1 (bases 1 to 43)	
	Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hulman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rikun,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.	
	The Washu-Merck EST Project	
	Unpublished (1995)	
TITLE	Contact: Wilson RK	
JOURNAL	Washington University School of Medicine	
COMMENT	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108	
	Tel: 314 286 1800	
	Fax: 314 286 1810	
	Email: est@watson.wustl.edu	
	Insert Size: 1223	
	High quality sequence starts: 1	
	High quality sequence stops: 1	
	Source: IMAGE Consortium, LBNL.	
	This clone is available royalty-free through LBNL; contact the	
	IMAGE Consortium (info@image.lbnl.gov) for further information.	
	Trace considered overall poor quality	

BASE COUNT
ORIGIN

10	a	13	c	10	g	16	t
----	---	----	---	----	---	----	---

	Query Match	58.9%	Score 10.6;	DB 9;	.length 49;
	Best Local Similarity	76.5%;	Pred. No. 4.1e+05;		
	Matches 13; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;
Oy	1 CCCGAGGCACCTCGG	17			
		11			
Db	39 CCAGAGGCACGTGTG	23			

RESULT 34	LOCUS	DEFINITION
AU108079/c	50 bp mRNA linear EST 30-AUG-2001	
AU108079	Sugano Homo sapiens cDNA library	
AU108079	ZR6C660, mRNA sequence.	

ACCESSION	AV108079	
VERSION	AV108079.1	GI:13557601
KEYWORDS	EST.	
SOURCE	human.	

ORGANISM	REFERENCE
Homo sapiens	
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;	
Mammalia: Eutheria: Primates: Catarrhini: Hominoideae; Homo.	
1 (bases 1 to 50)	
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hatake,	

TITLE	Diverse transcriptional initiation revealed by fine, large-scale
JOURNAL	mapping of mRNA start sites
MEDLINE	EMBO Rep. 2 (5), 388-393 (2001)
COMMENT	21270072
	Contact: Yutaka Suzuki

FEATURES
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Suganoc,
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. *gene* 200 (1-2), 149-156 (1997).
Location/Qualifiers

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ZRY6C660"
/clone_1lb="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfumarate treated u937 cells"
BASE COUNT      9 a      12 g      11 t
ORIGIN           17 c      1 others

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	Query Match	58.9%	Score 10.6	DB 9	Length 50
	Best Local Similarity	76.5%	Pred. No. 4.1e+05		
	Matches 13; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;
QY	2 CCGGAGGCAGTCTGGC	18			
db	33 CCTGAAGCCAGTGAGGC	17			

RESULT	35
BG296675	
LOCUS	50 bp mRNA linear EST 21-FEB-2001
DEFINITION	602393620F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4505500 5', mRNA sequence.
ACCESSION	BG296675
VERSION	BG296675.1 GI:13059564
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus

REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus
AUTHORS	1 (pages 1 to 50)
TITLE	NIH-MGC http://mgc.nhl.nih.gov/
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D.

email: cgapds-remail@nlb.gov
tissue Procurement: The Cepco Laboratory
CDNA library Preparation: Life Technologies, Inc.
CDNA library Arrayed by: the I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
plate: LLAM10379 row: g column: 05
high quality sequence stop: 50

FEATURES

```

/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:4505500"
/clone_1lb="NIH_MGC_94"
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/note="Origin: eye; Vector: pCMV-Sport6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies
Note: this is a NIH_MGC library."

```

[illegible]

RESULT 36	
AZ486623/c	
LOCUS	AZ486623
DEFINITION	22 bp DNA linear
	1M031161R1 Mouse 10kb plasmid U06C1M library Mus musculus genomic
	clone U06C1M0314G14 R, DNA sequence.

VERSION	AZ486623.1	GI:10653578
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	

REFERENCE	TITLE	JOURNAL	COMMENT
1 (bases 1 to 22)			
Dunn, D., Aoyagi, A., Barber, M., Baccorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	Unpublished (2000)	Contact: Robert B. Weiss

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0314 Row: G Column: 14
Seq primer: CACACAGGAACGCTATGACC

Class: plasmid ends	High quality sequence stop: 33
Location/Qualifiers	1. .33
FEATURES	
source	

BASE COUNT	8 a	11 c	4 g	10 t
ORIGIN				

Query Match	57.8%	Score 10.4;	DB 17;	Length 33;
Best Local Similarity	91.7%;	Pred. No. 4.8e+05;		
Matches 11; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

Qy	3	CGGAAGGCAGTC	14
Db	15	CGGTAGGCAGTC	4

RESULT	39				
LOCUS	AZ313241/c				
DEFINITION	AZ313241	35 bp	DNA	linear	GSS 29-SEP-2000
DESCRIPTION	IM0029H13R Mouse 10kb plasmid U0GC1M library Mus musculus genomic clone U0GC1M0029H13 R, DNA sequence.				

TITLE	Mouse whole genome scaffolding with paired end reads from 10xb
JOURNAL	plasmid inserts
COMMENT	Unpublished (2000)
	Contact: Robert B. Weiss

```

Class: plasmid ends
High quality sequence stop: 35.
Location/Qualifiers
1. .35
FEATURES
source
```

BASE COUNT	6 a	9 c	8 g	12 t
ORIGIN				

Query Match	57.8%;	Score 10.4;	DB 17;	Length 35;
Best Local Similarity	91.7%;	Pred. No. 4.9e+05;		
Matches 11; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

Qy	7	AGGCAGTCTGGC	18
Db	13	AGGCAGTGTGGC	2

RESULT 40	
A2607760/c	
LOCUS	A2607760 43 bp DNA linear GSS 13-DEC-2000
DEFINITION	IM0430F22F Mouse 10kb plasmid U06C1M library Mus musculus genomic clone U06C1M0430F22 F, DNA sequence.

TITLE	Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL	plasmid inserts
COMMENT	Unpublished (2000)
	Contact: Robert B. Weiss

Class: plasmid ends
High quality sequence stop: 43.
Location/Qualifiers
source

1. .43
/organism="Mus musculus"
/strain="C57BL/6J"
/db.xref="taxon:10090"
/clone="UUC1M0430P22"
/clone_1lb="mouse 10kb plasmid UUC1M library"
/sex="Male"
/lab_hosts="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g11473211419b/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into cells chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 14 a 9 c 8 g 12 t
ORIGIN

Query Match 57.8%; Score 10.4; DB 17; Length 43;
Best Local Similarity 91.7%; Pred. No. 5e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 GAAGCAGTCTG 16
|||||
Db 27 GAAGCATTCTG 16

Search completed: December 2, 2002, 14:06:30
Job time : 1968 secs

